

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 27.7352 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-167
Perfect score: 29
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
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- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	29	100.0	29	17	AAR88836		Human parathyroid
2	29	100.0	29	23	AAU73063		Parathyroid hormon
3	29	100.0	30	17	AAR88832		Human parathyroid
4	29	100.0	30	23	AAU73051		Parathyroid hormon
5	29	100.0	30	23	AAU73178		Parathyroid hormon
6	29	100.0	31	19	AAW42059		Human parathyroid
7	29	100.0	31	19	AAW42051		Human parathyroid
8	29	100.0	31	20	AAY02578		N-terminal 31 resi
9	29	100.0	31	22	AAB81080		Human parathyroid
10	29	100.0	31	22	AAB91097		Parathyroid hormon
11	29	100.0	31	23	AAE23720		Human parathyroid
12	29	100.0	31	23	AAU73039		Parathyroid hormon
13	29	100.0	31	23	AAU73177		Parathyroid hormon
14	29	100.0	32	23	AAU73176		Parathyroid hormon
15	29	100.0	33	21	AAY98018		Human amino-termin
16	29	100.0	34	4	AAP30022		Human parathyroid-
17	29	100.0	34	6	AAP50377		[Met (O)8,18]hPTH- (
18	29	100.0	34	7	AAP60031		Sequence of the fi
19	29	100.0	34	11	AAR07919		Human parathyroid
20	29	100.0	34	11	AAR07922		Human parathyroid
21	29	100.0	34	13	AAR22283		Parathyroid hormon
22	29	100.0	34	14	AAR41549		[D-Ser3]hPTH (1-34
23	29	100.0	34	14	AAR41570		[Gln25]hPTH (1-34)
24	29	100.0	34	15	AAR58291		[Lys (For)26, Lys (F
25	29	100.0	34	15	AAR58228		[D-Asp30]-hPTH(1-3
26	29	100.0	34	15	AAR58232		[Lys32]-hPTH(1-34)
27	29	100.0	34	15	AAR58181		[Thr33, Ala34]-hPT
28	29	100.0	34	15	AAR58016		N-alpha-Isopropyl-
29	29	100.0	34	15	AAR58017		[Lys (N-epsilon-Iso
30	29	100.0	34	15	AAR55724		Parathormone N-ter
31	29	100.0	34	16	AAR74521		Human parathyroid
32	29	100.0	34	17	AAW99449		Human parathyroid
33	29	100.0	34	17	AAR99978		Human parathyroid
34	29	100.0	34	17	AAR98951		Target peptide (PT
35	29	100.0	34	17	AAR98966		PTH(1-34). Not sp
36	29	100.0	34	17	AAR88835		Human parathyroid
37	29	100.0	34	18	AAW24273		Wild type parathyr
38	29	100.0	34	18	AAW19994		Cyclised human par
39	29	100.0	34	18	AAW20000		Cyclised human par
40	29	100.0	34	18	AAW20006		Cyclised human par
41	29	100.0	34	18	AAW17948		Human parathyroid
42	29	100.0	34	18	AAW17968		Human parathyroid
43	29	100.0	34	18	AAW17955		Human parathyroid
44	29	100.0	34	19	AAW67283		Parathyroid hormon
45	29	100.0	34	19	AAW67291		Parathyroid hormon
46	29	100.0	34	19	AAW61658		Parathyroid hormon
47	29	100.0	34	19	AAW65975		Human parathyroid
48	29	100.0	34	19	AAW42614		Human parathyroid
49	29	100.0	34	19	AAW48392		Human parathyroid
50	29	100.0	34	20	AAY50593		Resin bound cyclic

51	29	100.0	34	20	AA17752	Human parathyroid
52	29	100.0	34	20	AA14151	Human parathyroid
53	29	100.0	34	20	AA02579	N-terminal 34 resi
54	29	100.0	34	20	AAW81871	Human PTH N-termin
55	29	100.0	34	21	ABJ10712	Human parathyroid
56	29	100.0	34	21	AA07454	Amino acids 1-34 o
57	29	100.0	34	21	AA98017	Human amino-termin
58	29	100.0	34	21	AA82631	Human parathyroid
59	29	100.0	34	21	AA68763	Amino acids 1-34 o
60	29	100.0	34	22	AA84778	Native rat parathy
61	29	100.0	34	22	AA96898	Human parathyroid
62	29	100.0	34	22	AA96929	Human parathyroid
63	29	100.0	34	22	AA81079	Human parathyroid
64	29	100.0	34	22	AA91098	Parathyroid hormon
65	29	100.0	34	23	ABJ05328	Human PTH(1-34) pe
66	29	100.0	34	23	AAE23727	Human parathyroid
67	29	100.0	34	23	ABB06329	Human parathyroid
68	29	100.0	34	23	ABB08595	C-terminal truncat
69	29	100.0	34	23	AAE18395	Human PTH peptide
70	29	100.0	34	23	ABB07147	Parathyroid hormon
71	29	100.0	34	23	AAU73028	Parathyroid hormon
72	29	100.0	34	24	ABP71500	Human parathyroid
73	29	100.0	34	24	ABG74235	Human parathyroid
74	29	100.0	35	22	AA91112	Parathyroid hormon
75	29	100.0	35	23	AAU73172	Parathyroid hormon
76	29	100.0	36	14	AA39450	Ser-Val-(hPTH 3-35
77	29	100.0	36	15	AA58286	[D-Leu24]-hPTH(1-3
78	29	100.0	36	15	AA58292	[D-Lys27]-hPTH(1-3
79	29	100.0	36	15	AA58293	[D-Leu28]-hPTH(1-3
80	29	100.0	36	15	AA58294	[D-Phe34]-hPTH(1-3
81	29	100.0	36	15	AA58295	[D-Val35]-hPTH(1-3
82	29	100.0	36	15	AA58296	[Ala35]-hPTH(1-36)
83	29	100.0	36	15	AA58297	[Pro35]-hPTH(1-36)
84	29	100.0	36	15	AA58298	[NMeVal35]-hPTH(1-
85	29	100.0	36	15	AA58299	[Thr35,Ala36]-hPTH
86	29	100.0	36	15	AA58300	[D-Ala36]-hPTH(1-3
87	29	100.0	36	15	AA58301	[NMeAla36]-hPTH(1-
88	29	100.0	36	15	AA58260	[D-Val2]-hPTH(1-36
89	29	100.0	36	15	AA58263	[D-Ile5]-hPTH(1-36
90	29	100.0	36	15	AA58264	[D-Gln6]-hPTH(1-36
91	29	100.0	36	15	AA58265	[D-Leu7]-hPTH(1-36
92	29	100.0	36	15	AA58270	[D-Leu11]-hPTH(1-3
93	29	100.0	36	15	AA58272	[D-Lys13]-hPTH(1-3
94	29	100.0	36	15	AA58273	[D-Leu15]-hPTH(1-3
95	29	100.0	36	15	AA58276	[Met(O2)18]-hPTH(1
96	29	100.0	36	15	AA58278	[D-Met18]-hPTH(1-3
97	29	100.0	36	15	AA58280	[D-Arg20]-hPTH(1-3
98	29	100.0	36	15	AA58281	[D-Val21]-hPTH(1-3
99	29	100.0	36	15	AA58284	[D-Trp23]-hPTH(1-3
100	29	100.0	36	15	AA58227	[D-Gln29]-hPTH(1-3
101	29	100.0	36	15	AA58229	[Ala30]-hPTH(1-36)
102	29	100.0	36	15	AA58230	[D-Val31]-hPTH(1-3
103	29	100.0	36	15	AA58231	[Ala31]-hPTH(1-36)
104	29	100.0	36	15	AA58233	[D-His32]-hPTH(1-3
105	29	100.0	36	15	AA58234	[Ala32]-hPTH(1-36)
106	29	100.0	36	15	AA58235	[D-Asn33]-hPTH(1-3
107	29	100.0	36	15	AA58236	[Ala33]-hPTH(1-36)

108	29	100.0	36	15	AAR58237	[NMePhe34] -hPTH(1-
109	29	100.0	36	15	AAR58238	[D-Asp30] -hPTH(1-3
110	29	100.0	36	15	AAR58242	[Lys (Isopropyl) 13]
111	29	100.0	36	15	AAR58246	Acetyl-hPTH(1-36) -
112	29	100.0	36	15	AAR58249	[D-Ser1] -hPTH(1-36
113	29	100.0	36	15	AAR58191	[Ala34] -hPTH(1-36)
114	29	100.0	36	15	AAR58196	[D-Phe34, D-Ala36]
115	29	100.0	36	15	AAR58198	[D-Ser3] -hPTH(1-36
116	29	100.0	36	15	AAR58199	[D-Glu4] -hPTH(1-36
117	29	100.0	36	15	AAR58200	[D-His9] -hPTH(1-36
118	29	100.0	36	15	AAR58202	[D-Asn10] -hPTH(1-3
119	29	100.0	36	15	AAR58210	[D-His14] -hPTH(1-3
120	29	100.0	36	15	AAR58211	[D-Asn16] -hPTH(1-3
121	29	100.0	36	15	AAR58213	[D-Ser17] -hPTH(1-3
122	29	100.0	36	15	AAR58215	[D-Glu19] -hPTH(1-3
123	29	100.0	36	15	AAR58220	[D-Lys26] -hPTH(1-3
124	29	100.0	36	15	AAR58171	[N-Me-Ser1] -hPTH(1
125	29	100.0	37	12	AAR11882	Parathyroid hormon
126	29	100.0	37	13	AAR24778	hPTH(1-37) -amide/e
127	29	100.0	37	15	AAR58244	[Ala0] -hPTH(1-36) -
128	29	100.0	37	15	AAR58245	[Pro0] -hPTH(1-36) -
129	29	100.0	37	22	AAB86226	Human parathyroid
130	29	100.0	37	22	AAB86229	Human parathyroid
131	29	100.0	37	23	ABB82203	Human parathyroid
132	29	100.0	38	3	AAP20248	Parathyroid hormon
133	29	100.0	38	15	AAR58282	[Trp (SO2Pmc) 23] -hP
134	29	100.0	38	15	AAR58283	[Trp (Pmc) 23] -hPTH(
135	29	100.0	38	15	AAR58018	Isopropyl - [Lys (Iso
136	29	100.0	38	15	AAR58162	[Arg33] -hPTH(1-38)
137	29	100.0	38	15	AAR58163	[Pro33] -hPTH(1-38)
138	29	100.0	38	15	AAR58164	[Asp33] -hPTH(1-38)
139	29	100.0	38	15	AAR58165	[Ile33] -hPTH(1-38)
140	29	100.0	38	15	AAR58166	[Lys33] -hPTH(1-38)
141	29	100.0	38	15	AAR58167	[Ile31,Arg33] -hPTH
142	29	100.0	38	15	AAR58075	[Ser33] -hPTH(1-38)
143	29	100.0	38	15	AAR58076	[Thr33] -hPTH(1-38)
144	29	100.0	38	15	AAR58077	[Leu33] -hPTH(1-38)
145	29	100.0	38	15	AAR58078	[Gly33] -hPTH(1-38)
146	29	100.0	38	15	AAR58084	[Gln33] -hPTH(1-38)
147	29	100.0	38	15	AAR54234	PTH N-terminal. S
148	29	100.0	38	20	AAY02580	N-terminal 38 resi
149	29	100.0	38	22	AAB91101	Parathyroid hormon
150	29	100.0	38	23	AAE23729	Human parathyroid
151	29	100.0	38	23	AAE18400	Human PTH peptide
152	29	100.0	38	23	AAU73026	Parathyroid hormon
153	28	96.6	28	17	AAR88837	Human parathyroid
154	28	96.6	28	21	AAY98052	Human parathyroid
155	28	96.6	28	23	AAU73064	Parathyroid hormon
156	28	96.6	29	12	AAR11731	Adenine-rich PTH-(
157	28	96.6	29	23	AAU73179	Parathyroid hormon
158	28	96.6	30	23	AAU73055	Parathyroid hormon
159	28	96.6	33	21	AAY98012	Human amino-termin
160	28	96.6	33	21	AAY98015	Human amino-termin
161	28	96.6	34	18	AAW01610	Parathyroid hormon
162	28	96.6	34	19	AAW67293	Parathyroid hormon
163	28	96.6	34	21	AAY98010	Human amino-termin
164	28	96.6	34	21	AAY98011	Human amino-termin

165	28	96.6	34	21	AAAY98014	Human amino-termin
166	28	96.6	34	22	AAB911113	Parathyroid hormon
167	28	96.6	34	23	AAE23728	Human parathyroid
168	28	96.6	34	23	AAE18399	Human PTH peptide
169	28	96.6	34	23	AAU73032	Parathyroid hormon
170	28	96.6	36	12	AAR15842	Human parathyroid
171	28	96.6	36	13	AAR23995	Human paprthyroid
172	28	96.6	36	15	AAR58254	[4-aminosalicylic
173	28	96.6	36	15	AAR58255	[TMSA1]-hPTH(1-36)
174	28	96.6	36	15	AAR58256	[Phe1]-hPTH(1-36)-
175	28	96.6	36	15	AAR58257	[Propargylglycin1]
176	28	96.6	36	15	AAR58262	[Ala1]-hPTH(1-36)-
177	28	96.6	36	15	AAR58243	Propargyl-[Al1]-hPT
178	28	96.6	36	15	AAR58247	[Hyp1]-hPTH(1-36)-
179	28	96.6	36	15	AAR58248	N-Dimethyl-[Ala1]-
180	28	96.6	36	15	AAR58250	[Lys(For)1]-hPTH(1
181	28	96.6	36	15	AAR58251	[D-glyceric acid1]
182	28	96.6	36	15	AAR58252	[Asn1]-hPTH(1-36)-
183	28	96.6	36	15	AAR58253	[4-aminobenzoic ac
184	28	96.6	36	15	AAR58190	[Ala29]-hPTH(1-36)
185	28	96.6	36	15	AAR58169	[D-Prol]-hPTH(1-36
186	28	96.6	36	15	AAR58170	[Nval]-hPTH(1-36)-
187	28	96.6	36	15	AAR58172	[Indole-2-carboxyl
188	28	96.6	36	15	AAR58173	[Indole-3-carboxyl
189	28	96.6	36	15	AAR58174	[Pyridine-3-carbox
190	28	96.6	36	15	AAR58175	[Pyridine-2-carbox
191	28	96.6	36	15	AAR58176	[Hexahydropyridazi
192	28	96.6	36	15	AAR58177	[Morpholine-2-carb
193	28	96.6	36	15	AAR58178	[Prol]-hPTH(1-36)-
194	28	96.6	36	15	AAR58179	[Leu1]-hPTH(1-36)-
195	28	96.6	36	15	AAR58180	[Ile1]-hPTH(1-36)-
196	28	96.6	36	15	AAR58026	N-alpha-methyl[Ala
197	28	96.6	36	15	AAR58168	[1-amino-cyclopent
198	28	96.6	37	23	AAU73027	Parathyroid hormon
199	28	96.6	38	15	AAR58019	N-alpha-methyl[Ala
200	28	96.6	38	15	AAR58022	[Ile1]-hPTH(1-38)-
201	28	96.6	38	15	AAR58028	[Thr1]-hPTH(1-38)-
202	28	96.6	38	15	AAR58029	[Leu1]-hPTH(1-38)-
203	28	96.6	38	15	AAR58030	[Abu1 or Gaba1]-hP
204	27	93.1	28	21	AAAY98048	Human parathyroid
205	27	93.1	28	21	AAAY98050	Human parathyroid
206	27	93.1	32	5	AAP40427	Parathyroid antago
207	27	93.1	34	18	AAW17947	Human parathyroid
208	27	93.1	34	18	AAW17951	Human parathyroid
209	27	93.1	34	19	AAW67282	Parathyroid hormon
210	27	93.1	34	19	AAW67286	Parathyroid hormon
211	27	93.1	34	22	AAB61638	Peptide #1 that ca
212	27	93.1	36	15	AAR58259	[aBU2]-hPTH(1-36)-
213	27	93.1	36	15	AAR58261	[Tert.Leu]-hPTH(1-
214	27	93.1	38	15	AAR58023	[Ala1,Abu2 or Nva2
215	27	93.1	38	15	AAR58024	[Ala1,Ile2]-hPTH(1
216	27	93.1	38	15	AAR58159	[Val28]-hPTH(1-38)
217	27	93.1	38	15	AAR58160	[Ile28]-hPTH(1-38)
218	26	89.7	28	17	AAR88838	Human parathyroid
219	26	89.7	28	22	AAB81074	Human parathyroid
220	26	89.7	29	17	AAR88839	Human parathyroid
221	26	89.7	29	22	AAB81075	Human parathyroid

222	26	89.7	30	17	AAR88833	Human parathyroid
223	26	89.7	30	19	AAW42052	Human parathyroid
224	26	89.7	30	23	AAU73062	Parathyroid hormon
225	26	89.7	31	5	AAP40760	Human parathyroid
226	26	89.7	31	19	AAW42056	Human parathyroid
227	26	89.7	31	19	AAW42057	Human parathyroid
228	26	89.7	31	19	AAW42060	Human parathyroid
229	26	89.7	31	19	AAW42062	Human parathyroid
230	26	89.7	31	19	AAW42067	Human parathyroid
231	26	89.7	31	19	AAW42049	Human parathyroid
232	26	89.7	31	19	AAW42050	Human parathyroid
233	26	89.7	31	19	AAW42053	Human parathyroid
234	26	89.7	31	23	AAU73040	Parathyroid hormon
235	26	89.7	31	23	AAU82640	Analogue of human
236	26	89.7	34	13	AAR22298	Human parathyroid
237	26	89.7	34	13	AAR22299	Human parathyroid
238	26	89.7	34	14	AAR41550	[D-Ala3]hPTH (1-34
239	26	89.7	34	14	AAR41554	[Thr27]hPTH (1-34)
240	26	89.7	34	14	AAR41555	[Asn27]hPTH (1-34)
241	26	89.7	34	14	AAR41558	[Ser27]hPTH (1-34)
242	26	89.7	34	14	AAR41559	[Gly27]hPTH (1-34)
243	26	89.7	34	14	AAR41560	[His27]hPTH (1-34)
244	26	89.7	34	17	AAR88829	Human parathyroid
245	26	89.7	34	17	AAR88834	Human parathyroid
246	26	89.7	34	18	AAW17969	Human parathyroid
247	26	89.7	34	18	AAW17957	Human parathyroid
248	26	89.7	34	19	AAW67292	Parathyroid hormon
249	26	89.7	34	19	AAW67297	Parathyroid hormon
250	26	89.7	34	19	AAW42054	Human parathyroid
251	26	89.7	34	19	AAW42055	Human parathyroid
252	26	89.7	36	15	AAR58222	[His27]-hPTH(1-36)
253	26	89.7	36	15	AAR58223	[Phe27]-hPTH(1-36)
254	26	89.7	36	15	AAR58224	[Nle27]-hPTH(1-36)
255	26	89.7	36	15	AAR58225	[Asn27]-hPTH(1-36)
256	26	89.7	36	15	AAR58226	[Ala27]-hPTH(1-36)
257	26	89.7	36	15	AAR58197	[Ala3]-hPTH(1-36)-
258	26	89.7	38	15	AAR58154	[Val27]-hPTH(1-38)
259	26	89.7	38	15	AAR58155	[Ile27]-hPTH(1-38)
260	26	89.7	38	15	AAR58156	[Leu27]-hPTH(1-38)
261	26	89.7	38	15	AAR58157	[Arg27]-hPTH(1-38)
262	26	89.7	38	15	AAR58158	[Ala27]-hPTH(1-38)
263	26	89.7	38	15	AAR58161	[Pro3,Thr33]-hPTH(
264	25	86.2	30	23	AAE23752	Human parathyroid
265	25	86.2	32	23	AAE23735	Human parathyroid
266	25	86.2	34	14	AAR41556	[Gln26,27]hPTH (1-
267	25	86.2	34	14	AAR41566	[Arg 26,27]hPTH (1
268	25	86.2	34	14	AAR41567	[Gln26]hPTH (1-34)
269	25	86.2	36	15	AAR58290	[Ala26]-hPTH(1-36)
270	25	86.2	36	15	AAR58218	[Gln26]-hPTH(1-36)
271	25	86.2	36	15	AAR58219	[Nle26]-hPTH(1-36)
272	25	86.2	38	15	AAR58153	[Arg26]-hPTH(1-38)
273	24	82.8	34	14	AAR34456	Human parathyroid
274	24	82.8	34	14	AAR34457	Human parathyroid
275	24	82.8	34	14	AAR41557	[Gln25,26,27]hPTH
276	24	82.8	34	19	AAW67290	Parathyroid hormon
277	24	82.8	36	15	AAR58287	[Phe25]-hPTH(1-36)
278	24	82.8	36	15	AAR58288	[Lys25]-hPTH(1-36)

279	24	82.8	36	15	AAR58289	[Ala25]-hPTH(1-36)
280	24	82.8	36	15	AAR58192	[Gln25]-hPTH(1-36)
281	23	79.3	28	13	AAR22064	Modified hPTH(7-34
282	23	79.3	28	13	AAR22065	Modified [Tyr_34]h
283	23	79.3	28	23	AAE23734	Human parathyroid
284	23	79.3	28	23	AAU73044	Parathyroid hormon
285	23	79.3	32	21	AAB07468	Antigenic peptide
286	23	79.3	34	18	AAW17949	Human parathyroid
287	23	79.3	34	18	AAW17945	Human parathyroid
288	23	79.3	34	18	AAW17950	Human PTH analogue
289	23	79.3	34	18	AAW01609	Parathryoid hormon
290	23	79.3	34	19	AAW67280	Parathyroid hormon
291	23	79.3	34	19	AAW67284	Parathyroid hormon
292	23	79.3	34	19	AAW67285	Parathyroid hormon
293	23	79.3	34	19	AAW67288	Parathyroid hormon
294	23	79.3	34	19	AAW67289	Parathyroid hormon
295	23	79.3	34	19	AAW67294	Parathyroid hormon
296	23	79.3	34	19	AAW67295	Parathyroid hormon
297	23	79.3	34	19	AAW67296	Parathyroid hormon
298	23	79.3	34	19	AAW67303	Parathyroid hormon
299	23	79.3	38	17	AAR98958	Target peptide (PT
300	22	75.9	30	23	AAU73136	Parathyroid hormon
301	22	75.9	30	23	AAU73137	Parathyroid hormon
302	22	75.9	31	17	AAR88830	Human parathyroid
303	22	75.9	32	17	AAR88840	Human parathyroid
304	22	75.9	33	9	AAP82176	Sequence of parath
305	22	75.9	33	17	AAR88841	Human parathyroid
306	22	75.9	34	14	AAR34358	Human parathyroid
307	22	75.9	34	14	AAR34353	Human parathyroid
308	22	75.9	34	14	AAR34354	Human parathyroid
309	22	75.9	34	14	AAR34355	Human parathyroid
310	22	75.9	34	14	AAR34356	Human parathyroid
311	22	75.9	34	14	AAR34357	Human parathyroid
312	22	75.9	34	14	AAR34359	Human parathyroid
313	22	75.9	34	14	AAR34360	Human parathyroid
314	22	75.9	34	14	AAR34361	Human parathyroid
315	22	75.9	34	14	AAR34362	Human parathyroid
316	22	75.9	34	14	AAR34363	Human parathyroid
317	22	75.9	34	14	AAR34364	Human parathyroid
318	22	75.9	34	14	AAR34365	Human parathyroid
319	22	75.9	34	14	AAR34366	Human parathyroid
320	22	75.9	34	14	AAR34367	Human parathyroid
321	22	75.9	34	14	AAR34368	Human parathyroid
322	22	75.9	34	15	AAR58187	[Phe23,His25,His26
323	22	75.9	34	15	AAR58189	[F23,H25,H26,L27,I
324	22	75.9	34	18	AAW17943	Human parathyroid
325	22	75.9	34	18	AAW17944	Human parathyroid
326	22	75.9	34	19	AAW67278	Parathyroid hormon
327	22	75.9	34	19	AAW67279	Parathyroid hormon
328	22	75.9	34	22	AAB91085	Parathyroid hormon
329	22	75.9	34	23	AAU73100	Parathyroid hormon
330	22	75.9	34	23	AAU73101	Parathyroid hormon
331	22	75.9	36	15	AAR58285	[Ala23]-hPTH(1-36)
332	22	75.9	36	15	AAR58188	[Phe23]-hPTH(1-36)
333	21	72.4	28	21	ABJ10776	Human parathyroid
334	21	72.4	30	23	AAU73138	Parathyroid hormon
335	21	72.4	30	23	AAU73139	Parathyroid hormon

336	21	72.4	31	19	AAW42063	Human parathyroid
337	21	72.4	31	19	AAW42065	Human parathyroid
338	21	72.4	31	19	AAW42066	Human parathyroid
339	21	72.4	34	13	AAR22293	Human parathyroid
340	21	72.4	34	15	AAR49697	Sequence of varian
341	21	72.4	34	15	AAR49698	Sequence of varian
342	21	72.4	34	19	AAW67305	Parathyroid hormon
343	21	72.4	34	19	AAW67299	Parathyroid hormon
344	21	72.4	34	19	AAW67302	Parathyroid hormon
345	21	72.4	34	19	AAW67304	Parathyroid hormon
346	21	72.4	34	21	ABJ10706	Human parathyroid
347	21	72.4	34	21	ABJ10714	Human parathyroid
348	21	72.4	34	21	ABJ10717	Human parathyroid
349	21	72.4	34	21	ABJ10719	Human parathyroid
350	21	72.4	34	21	ABJ10722	Human parathyroid
351	21	72.4	34	21	ABJ10724	Human parathyroid
352	21	72.4	34	21	ABJ10727	Human parathyroid
353	21	72.4	34	21	ABJ10729	Human parathyroid
354	21	72.4	34	21	ABJ10730	Human parathyroid
355	21	72.4	34	21	ABJ10733	Human parathyroid
356	21	72.4	34	21	ABJ10736	Human parathyroid
357	21	72.4	34	21	ABJ10772	Human parathyroid
358	21	72.4	34	21	ABJ10773	Human parathyroid
359	21	72.4	34	23	AAU73102	Parathyroid hormon
360	21	72.4	34	23	AAU73103	Parathyroid hormon
361	21	72.4	34	23	AAU73104	Parathyroid hormon
362	21	72.4	34	23	AAU73140	Parathyroid hormon
363	21	72.4	36	15	AAR58266	[Nle8]-hPTH(1-36)-
364	21	72.4	36	15	AAR58267	[Phe8]-hPTH(1-36)-
365	21	72.4	36	15	AAR58268	[Cha8]-hPTH(1-36)-
366	21	72.4	36	15	AAR58217	[Ala22]-hPTH(1-36)
367	21	72.4	36	15	AAR58182	[Nva8]-hPTH(1-36)-
368	21	72.4	38	15	AAR58269	[Leu8]-hPTH(1-38)-
369	21	72.4	38	15	AAR58145	[Gly22]-hPTH(1-38)
370	21	72.4	38	15	AAR58146	[Leu22]-hPTH(1-38)
371	21	72.4	38	15	AAR58147	[His22]-hPTH(1-38)
372	21	72.4	38	15	AAR58148	[Ala22]-hPTH(1-38)
373	21	72.4	38	15	AAR58149	[Ile22]-hPTH(1-38)
374	21	72.4	38	15	AAR58150	[Val22]-hPTH(1-38)
375	21	72.4	38	15	AAR58151	[Ser22]-hPTH(1-38)
376	21	72.4	38	15	AAR58152	[Arg22]-hPTH(1-38)
377	20	69.0	34	18	AAW24276	Parathyroid hormon
378	20	69.0	36	15	AAR58216	[Ala21]-hPTH(1-36)
379	20	69.0	38	15	AAR58138	[Ala21]-hPTH(1-38)
380	20	69.0	38	15	AAR58139	[Gly21]-hPTH(1-38)
381	20	69.0	38	15	AAR58140	[Phe21]-hPTH(1-38)
382	20	69.0	38	15	AAR58141	[Leu21]-hPTH(1-38)
383	20	69.0	38	15	AAR58142	[Asn21]-hPTH(1-38)
384	20	69.0	38	15	AAR58143	[Gln21]-hPTH(1-38)
385	20	69.0	38	15	AAR58144	[Ser21]-hPTH(1-38)
386	19	65.5	31	17	AAR88831	Human parathyroid
387	19	65.5	34	17	AAW15812	[Trp(10)]-hPTH(1-3
388	19	65.5	34	18	AAW08120	Human PTH derivati
389	19	65.5	34	18	AAW08109	Human parathyroid
390	19	65.5	34	18	AAW08114	Human PTH derivati
391	19	65.5	34	18	AAW08118	Human PTH derivati
392	19	65.5	34	18	AAW08119	Human PTH derivati

393	19	65.5	36	15	AAR58279	[Lys20]-hPTH(1-36)
394	19	65.5	36	15	AAR58201	[Ala10]-hPTH(1-36)
395	19	65.5	38	15	AAR58137	[Phe20]-hPTH(1-38)
396	18	62.1	28	21	AAU98046	Human parathyroid
397	18	62.1	30	23	AAU73052	Parathyroid hormone
398	18	62.1	30	23	AAU73053	Parathyroid hormone
399	18	62.1	30	23	AAU73054	Parathyroid hormone
400	18	62.1	34	13	AAR22292	Human parathyroid
401	18	62.1	34	13	AAR22294	Human parathyroid
402	18	62.1	34	13	AAR22296	Human parathyroid
403	18	62.1	34	13	AAR22297	Human parathyroid
404	18	62.1	34	15	AAR58193	[L8,D10,K11,T33,A3
405	18	62.1	34	15	AAR58194	[A1,H5,L8,D10,K11,
406	18	62.1	34	18	AAW08108	Human parathyroid
407	18	62.1	34	18	AAW08113	Human PTH derivati
408	18	62.1	34	18	AAW08117	Human PTH derivati
409	18	62.1	34	18	AAW17941	Human parathyroid
410	18	62.1	34	18	AAW17939	Human parathyroid
411	18	62.1	34	18	AAW17954	Human parathyroid
412	18	62.1	34	19	AAW67274	Parathyroid hormone
413	18	62.1	34	19	AAW67276	Parathyroid hormone
414	18	62.1	34	21	ABJ10713	Human parathyroid
415	18	62.1	34	21	ABJ10737	Human parathyroid
416	18	62.1	34	21	ABJ10769	Human parathyroid
417	18	62.1	34	23	AAU73029	Parathyroid hormone
418	18	62.1	34	23	AAU73030	Parathyroid hormone
419	18	62.1	34	23	AAU73031	Parathyroid hormone
420	18	62.1	35	23	AAU73173	Parathyroid hormone
421	18	62.1	35	23	AAU73174	Parathyroid hormone
422	18	62.1	35	23	AAU73175	Parathyroid hormone
423	18	62.1	36	15	AAR58271	[Ala11]-hPTH(1-36)
424	18	62.1	36	15	AAR58214	[Ala19]-hPTH(1-36)
425	18	62.1	38	15	AAR58136	[Arg19]-hPTH(1-38)
426	18	62.1	38	15	AAR58123	[Ser19]-hPTH(1-38)
427	18	62.1	38	15	AAR58124	[Lys19]-hPTH(1-38)
428	18	62.1	38	15	AAR58125	[Leu19]-hPTH(1-38)
429	18	62.1	38	15	AAR58126	[Ala19]-hPTH(1-38)
430	18	62.1	38	15	AAR58127	[Tyr19]-hPTH(1-38)
431	18	62.1	38	15	AAR58128	[Met19]-hPTH(1-38)
432	18	62.1	38	15	AAR58129	[His19]-hPTH(1-38)
433	18	62.1	38	15	AAR58130	[Val19]-hPTH(1-38)
434	18	62.1	38	15	AAR58131	[Gly19]-hPTH(1-38)
435	18	62.1	38	15	AAR58132	[Pro19]-hPTH(1-38)
436	18	62.1	38	15	AAR58133	[Asp19]-hPTH(1-38)
437	18	62.1	38	15	AAR58134	[Ile19]-hPTH(1-38)
438	18	62.1	38	15	AAR58135	[Val19,Gln24]-hPTH
439	17	58.6	28	13	AAR22066	Modified [D-Trp_12
440	17	58.6	28	21	AAU98041	Human parathyroid
441	17	58.6	28	21	AAU98042	Human parathyroid
442	17	58.6	28	21	AAU98044	Human parathyroid
443	17	58.6	34	11	AAR08300	Human parathyroid
444	17	58.6	34	11	AAR08303	Human parathyroid
445	17	58.6	34	13	AAR22291	Human parathyroid
446	17	58.6	34	18	AAW08121	Human PTH derivati
447	17	58.6	34	18	AAW08115	Human PTH derivati
448	17	58.6	34	18	AAW08116	Human PTH derivati
449	17	58.6	34	18	AAW17959	Human parathyroid

450	17	58.6	34	19	AAW67298	Parathyroid hormon
451	17	58.6	34	19	AAW67300	Parathyroid hormon
452	17	58.6	34	19	AAW67301	Parathyroid hormon
453	17	58.6	34	21	ABJ10742	Human parathyroid
454	17	58.6	34	22	AAB84771	Parathyroid hormon
455	17	58.6	34	22	AAB84826	Parathyroid hormon
456	17	58.6	34	22	AAB96893	Rat parathyroid ho
457	17	58.6	34	22	AAB96916	Parathyroid hormon
458	17	58.6	34	22	AAB96919	Parathyroid hormon
459	17	58.6	34	22	AAB96930	Rat parathyroid ho
460	17	58.6	34	22	AAB91087	Parathyroid hormon
461	17	58.6	36	15	AAR58277	[Nle18]-hPTH(1-36)
462	17	58.6	36	15	AAR58203	[Ala12]-hPTH(1-36)
463	17	58.6	36	15	AAR58183	[Gln18]-hPTH(1-36)
464	17	58.6	36	15	AAR58184	[Tyr18]-hPTH(1-36)
465	17	58.6	36	15	AAR58185	[Lys18]-hPTH(1-36)
466	17	58.6	36	15	AAR58186	[Ala18]-hPTH(1-36)
467	17	58.6	38	15	AAR58089	[Arg12]-hPTH(1-38)
468	17	58.6	38	15	AAR58090	[Ser12]-hPTH(1-38)
469	16	55.2	28	22	AAB81078	Human parathyroid
470	16	55.2	28	23	AAU73105	Parathyroid hormon
471	16	55.2	28	23	AAU73106	Parathyroid hormon
472	16	55.2	30	6	AAP50665	Human parathyroid
473	16	55.2	31	22	AAB81077	Human parathyroid
474	16	55.2	34	17	AAW14310	Cyclic parathyroid
475	16	55.2	34	17	AAW14311	Cyclic parathyroid
476	16	55.2	34	18	AAW08112	Human PTH derivati
477	16	55.2	34	18	AAW17958	Human parathyroid
478	16	55.2	36	15	AAR58204	[Gln13]-hPTH(1-36)
479	16	55.2	36	15	AAR58205	[His13]-hPTH(1-36)
480	16	55.2	36	15	AAR58206	[Leu13]-hPTH(1-36)
481	16	55.2	36	15	AAR58207	[Ala13]-hPTH(1-36)
482	16	55.2	36	15	AAR58212	[Ala17]-hPTH(1-36)
483	16	55.2	38	15	AAR58091	[Cys13]-hPTH(1-38)
484	16	55.2	38	15	AAR58092	[Ile13]-hPTH(1-38)
485	16	55.2	38	15	AAR58093	[Asn13]-hPTH(1-38)
486	16	55.2	38	15	AAR58094	[Trp13]-hPTH(1-38)
487	16	55.2	38	15	AAR58095	[Asp13]-hPTH(1-38)
488	16	55.2	38	15	AAR58096	[Val13]-hPTH(1-38)
489	16	55.2	38	15	AAR58097	[Thr13]-hPTH(1-38)
490	16	55.2	38	15	AAR58098	[Ser13]-hPTH(1-38)
491	16	55.2	38	15	AAR58099	[Tyr13]-hPTH(1-38)
492	16	55.2	38	15	AAR58100	[Met13]-hPTH(1-38)
493	16	55.2	38	15	AAR58101	[Gln13]-hPTH(1-38)
494	16	55.2	38	15	AAR58102	[Leu13]-hPTH(1-38)
495	16	55.2	38	15	AAR58103	[Ala13]-hPTH(1-38)
496	16	55.2	38	15	AAR58104	[Gly13]-hPTH(1-38)
497	16	55.2	38	15	AAR58120	[Ala17]-hPTH(1-38)
498	16	55.2	38	15	AAR58121	[Met17]-hPTH(1-38)
499	16	55.2	38	15	AAR58122	[Ile17]-hPTH(1-38)
500	15	51.7	28	23	AAU73107	Parathyroid hormon
501	15	51.7	28	23	AAU73108	Parathyroid hormon
502	15	51.7	28	23	AAU73109	Parathyroid hormon
503	15	51.7	30	23	AAU73059	Parathyroid hormon
504	15	51.7	31	21	AAV96973	Parathyroid hormon
505	15	51.7	31	21	AAV96974	Parathyroid hormon
506	15	51.7	34	14	AAR41551	[Thr16]hPTH (1-34)

507	15	51.7	34	14	AAR41552	[Glu16]hPTH (1-34)
508	15	51.7	34	14	AAR41553	[Lys16]hPTH (1-34)
509	15	51.7	34	14	AAR41561	[Lys16, Gln27]hPTH
510	15	51.7	34	14	AAR41562	[Orn16, Gln27]hPTH
511	15	51.7	34	14	AAR41563	[Hci16, Gln27]hPTH
512	15	51.7	34	14	AAR41564	[Asp16, Gln27]hPTH
513	15	51.7	34	14	AAR41565	[Arg16, Gln27]hPTH
514	15	51.7	34	14	AAR41571	[D-Lys16]hPTH (1-3
515	15	51.7	34	14	AAR41573	[Gln16]hPTH (1-34)
516	15	51.7	34	14	AAR41574	[Ser16]hPTH (1-34)
517	15	51.7	34	14	AAR41575	[Gly16]hPTH (1-34)
518	15	51.7	34	14	AAR41576	[Lys16]hPTH (1-34)
519	15	51.7	34	14	AAR41577	[Lys16, Asp17]hPTH
520	15	51.7	34	14	AAR41580	[Lys16,17]hPTH (1-
521	15	51.7	34	14	AAR41581	[Arg16,17]hPTH (1-
522	15	51.7	34	17	AAR99981	Porcine parathyroi
523	15	51.7	34	18	AAW08129	Human PTH derivati
524	15	51.7	34	18	AAW08132	Human PTH derivati
525	15	51.7	34	18	AAW17967	Human PTH analogue
526	15	51.7	34	18	AAW17953	Human parathyroid
527	15	51.7	34	18	AAW17956	Human parathyroid
528	15	51.7	34	19	AAW61660	Parathyroid hormon
529	15	51.7	34	19	AAW65977	Porcine parathyroi
530	15	51.7	34	19	AAW42616	Porcine parathyroi
531	15	51.7	34	19	AAW48394	Human PTH/PTHrP hy
532	15	51.7	34	20	AAW81873	Porcine PTH N-term
533	15	51.7	34	22	AAB84775	Parathyroid hormon
534	15	51.7	34	22	AAB96922	Parathyroid hormon
535	15	51.7	34	23	AAU73036	Parathyroid hormon
536	15	51.7	36	15	AAR58275	[Ala16]-hPTH(1-36)
537	15	51.7	36	15	AAR58209	[Ala14]-hPTH(1-36)
538	15	51.7	37	22	AAB86232	Porcine parathyroi
539	15	51.7	38	15	AAR58036	[Gln16]-hPTH(1-38)
540	15	51.7	38	15	AAR58037	[Ser14]-hPTH(1-38)
541	15	51.7	38	15	AAR58105	[Val14]-hPTH(1-38)
542	15	51.7	38	15	AAR58106	[Ala14]-hPTH(1-38)
543	15	51.7	38	15	AAR58107	[Lys14]-hPTH(1-38)
544	15	51.7	38	15	AAR58108	[Arg14]-hPTH(1-38)
545	15	51.7	38	15	AAR58109	[Thr14]-hPTH(1-38)
546	15	51.7	38	15	AAR58110	[Ile14]-hPTH(1-38)
547	15	51.7	38	15	AAR58111	[Tyr14]-hPTH(1-38)
548	15	51.7	38	15	AAR58115	[Lys16]-hPTH(1-38)
549	15	51.7	38	15	AAR58116	[Ser16]-hPTH(1-38)
550	15	51.7	38	15	AAR58117	[Leu16]-hPTH(1-38)
551	15	51.7	38	15	AAR58118	[Ala16]-hPTH(1-38)
552	15	51.7	38	15	AAR58119	[Gly16]-hPTH(1-38)
553	14	48.3	30	23	AAU73060	Parathyroid hormon
554	14	48.3	34	9	AAP82177	Sequence of parath
555	14	48.3	34	11	AAR07917	Rat parathyroid ho
556	14	48.3	34	11	AAR07920	Rat parathyroid ho
557	14	48.3	34	14	AAR41568	[Lys15,16 His27]hP
558	14	48.3	34	14	AAR41569	[Lys15, His27]hPTH
559	14	48.3	34	14	AAR41572	[Lys15,16,17, His2
560	14	48.3	34	14	AAR41579	[Lys15,15,17]hPTH
561	14	48.3	34	14	AAR41582	[Arg15,16,17]hPTH
562	14	48.3	34	16	AAR62432	Accelerator peptid
563	14	48.3	34	17	AAR99980	Rat parathyroid ho

564	14	48.3	34	18	AAW19996	Cyclised rat parat
565	14	48.3	34	18	AAW20002	Cyclised rat parat
566	14	48.3	34	18	AAW20008	Cyclised rat parat
567	14	48.3	34	18	AAW17942	Human parathyroid
568	14	48.3	34	18	AAW17952	Human parathyroid
569	14	48.3	34	19	AAW67277	Parathyroid hormon
570	14	48.3	34	19	AAW67287	Parathyroid hormon
571	14	48.3	34	19	AAW48398	Human PTH/PTHrP hy
572	14	48.3	34	22	AAB84777	Native human parat
573	14	48.3	34	22	AAB96897	Rat parathyroid ho
574	14	48.3	34	22	AAB91100	Parathyroid hormon
575	14	48.3	34	23	AAU73037	Parathyroid hormon
576	14	48.3	34	24	ABP71489	Parathyroid hormon
577	14	48.3	34	24	ABP71499	Rat parathyroid ho
578	14	48.3	36	15	AAR58274	[Ala15]-hPTH(1-36)
579	14	48.3	36	15	AAR58071	[Aib3, Gln18]-hPTH
580	14	48.3	36	15	AAR58088	[1-amino-cyclopent
581	14	48.3	37	22	AAB86231	Rat parathyroid ho
582	14	48.3	38	15	AAR58061	[Ile15]-hPTH(1-38)
583	14	48.3	38	15	AAR58112	[Tyr15]-hPTH(1-38)
584	14	48.3	38	15	AAR58113	[Arg15]-hPTH(1-38)
585	14	48.3	38	15	AAR58114	[Val15]-hPTH(1-38)
586	13	44.8	28	13	AAR22058	Modified bovine PT
587	13	44.8	28	13	AAR22059	Modified [Tyr_34]b
588	13	44.8	28	13	AAR22060	Modified [D-Trp_12
589	13	44.8	28	22	AAB91115	Parathyroid hormon
590	13	44.8	28	23	AAE18405	Bovine PTH peptide
591	13	44.8	28	23	AAU73046	Parathyroid hormon
592	13	44.8	28	23	AAU73047	Parathyroid hormon
593	13	44.8	28	23	AAU73050	Parathyroid hormon
594	13	44.8	28	23	AAU73066	Parathyroid hormon
595	13	44.8	30	23	AAU73057	Parathyroid hormon
596	13	44.8	31	5	AAP40510	Bovine parathyroid
597	13	44.8	31	21	AAV96975	Parathyroid hormon
598	13	44.8	32	22	AAB91096	Parathyroid hormon
599	13	44.8	32	23	AAE23739	Bovine parathyroid
600	13	44.8	32	23	AAE18402	Bovine PTH peptide
601	13	44.8	32	23	AAU73042	Parathyroid hormon
602	13	44.8	34	11	AAR07918	Bovine parathyroid
603	13	44.8	34	11	AAR07921	Bovine parathyroid
604	13	44.8	34	11	AAR08299	Bovine parathyroid
605	13	44.8	34	11	AAR08302	Bovine parathyroid
606	13	44.8	34	14	AAR41578	[Lys14,15,16,17]hP
607	13	44.8	34	15	AAR58195	[S14,I15,Q16,D17,L
608	13	44.8	34	17	AAR99979	Bovine parathyroid
609	13	44.8	34	18	AAW08124	Human PTH derivati
610	13	44.8	34	18	AAW08111	Human PTH derivati
611	13	44.8	34	18	AAW19995	Cyclised bovine pa
612	13	44.8	34	18	AAW20001	Cyclised bovine pa
613	13	44.8	34	18	AAW20007	Cyclised bovine pa
614	13	44.8	34	18	AAW17963	Human PTH analogue
615	13	44.8	34	19	AAW61659	Parathyroid hormon
616	13	44.8	34	19	AAW65976	Bovine parathyroid
617	13	44.8	34	19	AAW42615	Bovine parathyroid
618	13	44.8	34	20	AAW81872	Bovine PTH N-termi
619	13	44.8	34	23	AAE23738	Bovine parathyroid
620	13	44.8	34	23	AAE18394	Bovine PTH peptide

621	13	44.8	34	23	AAU73034	Parathyroid hormon
622	13	44.8	37	22	AAB86230	Bovine parathyroid
623	13	44.8	37	22	AAB86233	Canine parathyroid
624	13	44.8	37	23	ABB82204	Bovine parathyroid
625	12	41.4	34	14	AAV18002	Human PTH(1-34) de
626	12	41.4	34	17	AAW14308	Cyclic parathyroid
627	12	41.4	34	17	AAW14309	Cyclic parathyroid
628	12	41.4	34	17	AAW14312	Cyclic parathyroid
629	12	41.4	34	17	AAW14313	Cyclic parathyroid
630	12	41.4	34	17	AAW14314	Cyclic parathyroid
631	12	41.4	34	17	AAW14315	Cyclic parathyroid
632	12	41.4	34	18	AAW08122	Human PTH derivati
633	12	41.4	34	18	AAW08123	Human PTH derivati
634	12	41.4	34	20	AAV03923	Analogue of parath
635	12	41.4	34	20	AAV03919	Analogue of parath
636	12	41.4	34	24	ABP71490	Parathyroid hormon
637	12	41.4	34	24	ABP71491	Parathyroid hormon
638	12	41.4	34	24	ABP71492	Parathyroid hormon
639	12	41.4	34	24	ABP71494	Parathyroid hormon
640	12	41.4	36	15	AAR58208	[A13,Q26,F27,D-F34
641	11	37.9	28	13	AAR22061	Modified [Nle_8,18
642	11	37.9	28	13	AAR22062	Modified [Nle_8,18
643	11	37.9	28	13	AAR22067	Modified [Nle_8,_1
644	11	37.9	28	13	AAR22068	Modified [Nle_8,_1
645	11	37.9	28	21	ABJ10774	Human parathyroid
646	11	37.9	28	21	ABJ10775	Human parathyroid
647	11	37.9	28	23	AAE18404	Bovine PTH peptide
648	11	37.9	28	23	AAU73045	Parathyroid hormon
649	11	37.9	28	23	AAU73048	Parathyroid hormon
650	11	37.9	28	23	AAU73049	Parathyroid hormon
651	11	37.9	28	23	AAU73065	Parathyroid hormon
652	11	37.9	28	23	AAU73067	Parathyroid hormon
653	11	37.9	30	22	AAB91089	Parathyroid hormon
654	11	37.9	30	22	AAB91092	Parathyroid hormon
655	11	37.9	30	23	AAU73056	Parathyroid hormon
656	11	37.9	30	23	AAU73058	Parathyroid hormon
657	11	37.9	31	5	AAP40511	Bovine parathyroid
658	11	37.9	31	5	AAP40761	Human parathyroid
659	11	37.9	32	12	AAR14726	Human parathyroid
660	11	37.9	32	22	AAB91088	Parathyroid hormon
661	11	37.9	32	22	AAB91090	Parathyroid hormon
662	11	37.9	32	22	AAB91091	Parathyroid hormon
663	11	37.9	32	23	AAE18403	Bovine PTH peptide
664	11	37.9	32	23	AAU73041	Parathyroid hormon
665	11	37.9	32	23	AAU73043	Parathyroid hormon
666	11	37.9	33	17	AAW15814	[Leu(8),Trp(10),Al
667	11	37.9	34	6	AAP50517	Sequence of methio
668	11	37.9	34	11	AAR07924	Bovine parathyroid
669	11	37.9	34	11	AAR07925	Human parathyroid
670	11	37.9	34	11	AAR08305	Bovine parathyroid
671	11	37.9	34	11	AAR08306	Human parathyroid
672	11	37.9	34	13	AAR22295	Human parathyroid
673	11	37.9	34	15	AAR45528	Parathyroid hormon
674	11	37.9	34	15	AAR58239	Isopropyl- [Nle8,18
675	11	37.9	34	15	AAR58241	[Nle8,18,D-Asn33,D
676	11	37.9	34	15	AAR55817	[L8,Q18,T33,A34] -h
677	11	37.9	34	15	AAR55819	[L8,A16,Q18,T33,A3

678	11	37.9	34	15	AAR55821	[L8,D10,K11,Q18,T3
679	11	37.9	34	15	AAR55823	[L8,D10,K11,A16,Q1
680	11	37.9	34	15	AAR58021	[L8,D10,A16,Q18,T3
681	11	37.9	34	15	AAR58034	Isopropyl-[L8,K(Is
682	11	37.9	34	16	AAR69055	PTH analogue with
683	11	37.9	34	17	AAW15813	[Leu(8),Trp(10),Al
684	11	37.9	34	17	AAW15815	[Leu(8),Trp(10),DL
685	11	37.9	34	17	AAW15828	N-alpha-acylated [
686	11	37.9	34	17	AAW14316	Cyclic parathyroid
687	11	37.9	34	18	AAW13352	Truncated parathyr
688	11	37.9	34	18	AAW12651	Parathyroid hormon
689	11	37.9	34	18	AAW20004	Cyclised [Nle 8,18
690	11	37.9	34	18	AAW19997	Cyclised [Nle 8,18
691	11	37.9	34	18	AAW19998	Cyclised [Nle 8,18
692	11	37.9	34	18	AAW20003	Cyclised [Nle 8,18
693	11	37.9	34	18	AAW20009	Cyclised [Nle 8,18
694	11	37.9	34	18	AAW20010	Cyclised [Nle 8,18
695	11	37.9	34	18	AAW17940	Human PTH analogue
696	11	37.9	34	18	AAW17970	Human PTH analogue
697	11	37.9	34	18	AAW17964	Human PTH analogue
698	11	37.9	34	19	AAW67275	Parathyroid hormon
699	11	37.9	34	19	AAW61725	Parathyroid hormon
700	11	37.9	34	19	AAW66053	Parathyroid hormon
701	11	37.9	34	19	AAW42602	Parathyroid hormon
702	11	37.9	34	19	AAW48395	Human PTH/PTHrP hy
703	11	37.9	34	20	AAW02587	Parathyroid hormon
704	11	37.9	34	20	AAW92218	Analogue of parath
705	11	37.9	34	20	AAW92219	Analogue of parath
706	11	37.9	34	20	AAW03920	Analogue of parath
707	11	37.9	34	20	AAW03921	Analogue of parath
708	11	37.9	34	20	AAW03922	Analogue of parath
709	11	37.9	34	20	AAW03924	Analogue of parath
710	11	37.9	34	20	AAW03925	Analogue of parath
711	11	37.9	34	20	AAW03926	Analogue of parath
712	11	37.9	34	20	AAW03927	Analogue of parath
713	11	37.9	34	20	AAW03928	Analogue of parath
714	11	37.9	34	20	AAW03929	Analogue of parath
715	11	37.9	34	20	AAW03930	Analogue of parath
716	11	37.9	34	20	AAW03931	Analogue of parath
717	11	37.9	34	20	AAW03932	Analogue of parath
718	11	37.9	34	20	AAW03933	Analogue of parath
719	11	37.9	34	20	AAW92236	Analogue of parath
720	11	37.9	34	20	AAW92237	Analogue of parath
721	11	37.9	34	20	AAW92238	Analogue of parath
722	11	37.9	34	20	AAW92239	Analogue of parath
723	11	37.9	34	20	AAW92240	Analogue of parath
724	11	37.9	34	20	AAW92241	Analogue of parath
725	11	37.9	34	20	AAW92242	Analogue of parath
726	11	37.9	34	20	AAW92243	Analogue of parath
727	11	37.9	34	20	AAW92244	Analogue of parath
728	11	37.9	34	20	AAW92245	Analogue of parath
729	11	37.9	34	20	AAW92246	Analogue of parath
730	11	37.9	34	20	AAW92247	Analogue of parath
731	11	37.9	34	20	AAW92248	Analogue of parath
732	11	37.9	34	20	AAW92249	Analogue of parath
733	11	37.9	34	20	AAW92250	Analogue of parath
734	11	37.9	34	20	AAW92220	Analogue of parath

735	11	37.9	34	20	AAW92221	Analogue of parath
736	11	37.9	34	20	AAW92222	Analogue of parath
737	11	37.9	34	20	AAW92223	Analogue of parath
738	11	37.9	34	20	AAW92224	Analogue of parath
739	11	37.9	34	20	AAW92225	Analogue of parath
740	11	37.9	34	20	AAW92226	Analogue of parath
741	11	37.9	34	20	AAW92227	Analogue of parath
742	11	37.9	34	20	AAW92228	Analogue of parath
743	11	37.9	34	20	AAW92229	Analogue of parath
744	11	37.9	34	20	AAW92230	Analogue of parath
745	11	37.9	34	20	AAW92231	Analogue of parath
746	11	37.9	34	20	AAW92232	Analogue of parath
747	11	37.9	34	20	AAW92233	Analogue of parath
748	11	37.9	34	20	AAW92234	Analogue of parath
749	11	37.9	34	20	AAW92235	Analogue of parath
750	11	37.9	34	20	AAW92236	Analogue of parath
751	11	37.9	34	20	AAW92237	Analogue of parath
752	11	37.9	34	20	AAW92238	Analogue of parath
753	11	37.9	34	20	AAW92239	Analogue of parath
754	11	37.9	34	20	AAW92240	Analogue of parath
755	11	37.9	34	20	AAW92241	Analogue of parath
756	11	37.9	34	20	AAW92242	Analogue of parath
757	11	37.9	34	20	AAW92243	Analogue of parath
758	11	37.9	34	20	AAW92244	Analogue of parath
759	11	37.9	34	20	AAW92245	Analogue of parath
760	11	37.9	34	20	AAW92246	Analogue of parath
761	11	37.9	34	20	AAW92247	Analogue of parath
762	11	37.9	34	20	AAW92248	Analogue of parath
763	11	37.9	34	20	AAW92249	Analogue of parath
764	11	37.9	34	20	AAW92250	Analogue of parath
765	11	37.9	34	20	AAW92251	Analogue of parath
766	11	37.9	34	20	AAW92252	Analogue of parath
767	11	37.9	34	20	AAW92253	Analogue of parath
768	11	37.9	34	20	AAW92254	Analogue of parath
769	11	37.9	34	20	AAW92255	Analogue of parath
770	11	37.9	34	20	AAW92256	Analogue of parath
771	11	37.9	34	20	AAW92257	Analogue of parath
772	11	37.9	34	20	AAW92258	Analogue of parath
773	11	37.9	34	20	AAW92259	Analogue of parath
774	11	37.9	34	20	AAW92260	Analogue of parath
775	11	37.9	34	20	AAW92261	Analogue of parath
776	11	37.9	34	20	AAW92262	Analogue of parath
777	11	37.9	34	20	AAW92263	Analogue of parath
778	11	37.9	34	20	AAW92264	Analogue of parath
779	11	37.9	34	20	AAW92265	Analogue of parath
780	11	37.9	34	20	AAW92266	Analogue of parath
781	11	37.9	34	20	AAW92267	Analogue of parath
782	11	37.9	34	20	AAW92268	Analogue of parath
783	11	37.9	34	20	AAW92269	Analogue of parath
784	11	37.9	34	20	AAW92270	Analogue of parath
785	11	37.9	34	20	AAW92271	Analogue of parath
786	11	37.9	34	20	AAW92272	Analogue of parath
787	11	37.9	34	20	AAW92273	Analogue of parath
788	11	37.9	34	20	AAW92274	Analogue of parath
789	11	37.9	34	20	AAW92275	Analogue of parath
790	11	37.9	34	20	AAW92276	Analogue of parath
791	11	37.9	34	20	AAW92277	Analogue of parath

792	11	37.9	34	20	AAW92202	Analogue of parath
793	11	37.9	34	20	AAW92183	Analogue of parath
794	11	37.9	34	20	AAW92184	Analogue of parath
795	11	37.9	34	20	AAW92185	Analogue of parath
796	11	37.9	34	20	AAW92186	Analogue of parath
797	11	37.9	34	20	AAW92187	Analogue of parath
798	11	37.9	34	20	AAW92167	Analogue of parath
799	11	37.9	34	20	AAW92188	Analogue of parath
800	11	37.9	34	20	AAW92189	Analogue of parath
801	11	37.9	34	20	AAW92190	Analogue of parath
802	11	37.9	34	20	AAW92191	Analogue of parath
803	11	37.9	34	20	AAW92192	Analogue of parath
804	11	37.9	34	20	AAW92193	Analogue of parath
805	11	37.9	34	20	AAW92194	Analogue of parath
806	11	37.9	34	20	AAW92195	Analogue of parath
807	11	37.9	34	20	AAW92196	Analogue of parath
808	11	37.9	34	20	AAW92197	Analogue of parath
809	11	37.9	34	20	AAW92166	Analogue of parath
810	11	37.9	34	20	AAW92168	Analogue of parath
811	11	37.9	34	20	AAW92169	Analogue of parath
812	11	37.9	34	20	AAW92170	Analogue of parath
813	11	37.9	34	20	AAW92171	Analogue of parath
814	11	37.9	34	20	AAW92172	Analogue of parath
815	11	37.9	34	20	AAW92173	Analogue of parath
816	11	37.9	34	20	AAW92174	Analogue of parath
817	11	37.9	34	20	AAW92175	Analogue of parath
818	11	37.9	34	20	AAW92176	Analogue of parath
819	11	37.9	34	20	AAW92177	Analogue of parath
820	11	37.9	34	20	AAW92178	Analogue of parath
821	11	37.9	34	20	AAW92179	Analogue of parath
822	11	37.9	34	20	AAW92180	Analogue of parath
823	11	37.9	34	20	AAW92181	Analogue of parath
824	11	37.9	34	20	AAW92182	Analogue of parath
825	11	37.9	34	20	AAW92152	Analogue of parath
826	11	37.9	34	20	AAW92150	Analogue of parath
827	11	37.9	34	20	AAW92151	Analogue of parath
828	11	37.9	34	20	AAW92153	Analogue of parath
829	11	37.9	34	20	AAW92154	Analogue of parath
830	11	37.9	34	20	AAW92155	Analogue of parath
831	11	37.9	34	20	AAW92156	Analogue of parath
832	11	37.9	34	20	AAW92157	Analogue of parath
833	11	37.9	34	20	AAW92158	Analogue of parath
834	11	37.9	34	20	AAW92159	Analogue of parath
835	11	37.9	34	20	AAW92160	Analogue of parath
836	11	37.9	34	20	AAW92161	Analogue of parath
837	11	37.9	34	20	AAW92162	Analogue of parath
838	11	37.9	34	20	AAW92163	Analogue of parath
839	11	37.9	34	20	AAW92164	Analogue of parath
840	11	37.9	34	20	AAW92165	Analogue of parath
841	11	37.9	34	20	AAW92148	Analogue of parath
842	11	37.9	34	20	AAW92149	Analogue of parath
843	11	37.9	34	20	AAW74396	Modified parathyro
844	11	37.9	34	20	AAW81945	Synthetic PTH and
845	11	37.9	34	21	ABJ10705	Human parathyroid
846	11	37.9	34	21	ABJ10707	Human parathyroid
847	11	37.9	34	21	ABJ10708	Human parathyroid
848	11	37.9	34	21	ABJ10709	Human parathyroid

849	11	37.9	34	21	ABJ10710	Human parathyroid
850	11	37.9	34	21	ABJ10711	Human parathyroid
851	11	37.9	34	21	ABJ10715	Human parathyroid
852	11	37.9	34	21	ABJ10716	Human parathyroid
853	11	37.9	34	21	ABJ10718	Human parathyroid
854	11	37.9	34	21	ABJ10720	Human parathyroid
855	11	37.9	34	21	ABJ10721	Human parathyroid
856	11	37.9	34	21	ABJ10723	Human parathyroid
857	11	37.9	34	21	ABJ10725	Human parathyroid
858	11	37.9	34	21	ABJ10726	Human parathyroid
859	11	37.9	34	21	ABJ10728	Human parathyroid
860	11	37.9	34	21	ABJ10731	Human parathyroid
861	11	37.9	34	21	ABJ10732	Human parathyroid
862	11	37.9	34	21	ABJ10734	Human parathyroid
863	11	37.9	34	21	ABJ10735	Human parathyroid
864	11	37.9	34	21	ABJ10738	Human parathyroid
865	11	37.9	34	21	ABJ10739	Human parathyroid
866	11	37.9	34	21	ABJ10740	Human parathyroid
867	11	37.9	34	21	ABJ10741	Human parathyroid
868	11	37.9	34	21	ABJ10743	Human parathyroid
869	11	37.9	34	21	ABJ10744	Human parathyroid
870	11	37.9	34	21	ABJ10745	Human parathyroid
871	11	37.9	34	21	ABJ10746	Human parathyroid
872	11	37.9	34	21	ABJ10747	Human parathyroid
873	11	37.9	34	21	ABJ10748	Human parathyroid
874	11	37.9	34	21	ABJ10749	Human parathyroid
875	11	37.9	34	21	ABJ10750	Human parathyroid
876	11	37.9	34	21	ABJ10751	Human parathyroid
877	11	37.9	34	21	ABJ10752	Human parathyroid
878	11	37.9	34	21	ABJ10753	Human parathyroid
879	11	37.9	34	21	ABJ10754	Human parathyroid
880	11	37.9	34	21	ABJ10755	Human parathyroid
881	11	37.9	34	21	ABJ10756	Human parathyroid
882	11	37.9	34	21	ABJ10761	Human parathyroid
883	11	37.9	34	21	ABJ10762	Human parathyroid
884	11	37.9	34	21	ABJ10763	Human parathyroid
885	11	37.9	34	21	ABJ10764	Human parathyroid
886	11	37.9	34	21	ABJ10765	Human parathyroid
887	11	37.9	34	21	ABJ10766	Human parathyroid
888	11	37.9	34	21	ABJ10767	Human parathyroid
889	11	37.9	34	21	ABJ10768	Human parathyroid
890	11	37.9	34	21	ABJ10771	Human parathyroid
891	11	37.9	34	21	ABJ10777	Human parathyroid
892	11	37.9	34	22	AAB91084	Parathyroid hormon
893	11	37.9	34	23	AAE18396	Bovine PTH peptide
894	11	37.9	34	23	AAE18397	Human PTH peptide
895	11	37.9	34	23	AAU73033	Parathyroid hormon
896	11	37.9	34	23	AAU73035	Parathyroid hormon
897	11	37.9	35	2	AAP10140	h-PTH antigen. Sy
898	11	37.9	35	16	AAR74512	Parathyroid hormon
899	11	37.9	35	16	AAR74513	Parathyroid hormon
900	11	37.9	35	16	AAR74514	Parathyroid hormon
901	11	37.9	35	16	AAR74515	Parathyroid hormon
902	11	37.9	35	16	AAR74516	Parathyroid hormon
903	11	37.9	35	16	AAR74517	Parathyroid hormon
904	11	37.9	35	16	AAR74518	Parathyroid hormon
905	11	37.9	35	16	AAR74519	Parathyroid hormon

906	11	37.9	35	16	AAR74520	Parathyroid hormon
907	11	37.9	35	16	AAR74527	Human parathyroid
908	11	37.9	35	16	AAR74506	Parathyroid hormon
909	11	37.9	35	16	AAR74507	Parathyroid hormon
910	11	37.9	35	16	AAR74508	Parathyroid hormon
911	11	37.9	35	16	AAR74509	Parathyroid hormon
912	11	37.9	35	16	AAR74510	Parathyroid hormon
913	11	37.9	35	16	AAR74511	Parathyroid hormon
914	11	37.9	35	16	AAR74464	Parathyroid hormon
915	11	37.9	35	16	AAR74465	Parathyroid hormon
916	11	37.9	35	16	AAR74466	Parathyroid hormon
917	11	37.9	35	16	AAR74467	Parathyroid hormon
918	11	37.9	35	16	AAR74468	Parathyroid hormon
919	11	37.9	35	16	AAR74469	Parathyroid hormon
920	11	37.9	35	16	AAR74470	Parathyroid hormon
921	11	37.9	35	16	AAR74471	Parathyroid hormon
922	11	37.9	35	16	AAR74472	Parathyroid hormon
923	11	37.9	35	16	AAR74473	Parathyroid hormon
924	11	37.9	35	16	AAR74474	Parathyroid hormon
925	11	37.9	35	16	AAR74475	Parathyroid hormon
926	11	37.9	35	16	AAR74476	Parathyroid hormon
927	11	37.9	35	16	AAR74477	Parathyroid hormon
928	11	37.9	35	16	AAR74478	Parathyroid hormon
929	11	37.9	35	16	AAR74479	Parathyroid hormon
930	11	37.9	35	16	AAR74448	Parathyroid hormon
931	11	37.9	35	16	AAR74449	Parathyroid hormon
932	11	37.9	35	16	AAR74450	Parathyroid hormon
933	11	37.9	35	16	AAR74451	Parathyroid hormon
934	11	37.9	35	16	AAR74452	Parathyroid hormon
935	11	37.9	35	16	AAR74453	Parathyroid hormon
936	11	37.9	35	16	AAR74454	Parathyroid hormon
937	11	37.9	35	16	AAR74455	Parathyroid hormon
938	11	37.9	35	16	AAR74456	Parathyroid hormon
939	11	37.9	35	16	AAR74457	Parathyroid hormon
940	11	37.9	35	16	AAR74458	Parathyroid hormon
941	11	37.9	35	16	AAR74459	Parathyroid hormon
942	11	37.9	35	16	AAR74460	Parathyroid hormon
943	11	37.9	35	16	AAR74461	Parathyroid hormon
944	11	37.9	35	16	AAR74462	Parathyroid hormon
945	11	37.9	35	16	AAR74463	Parathyroid hormon
946	11	37.9	35	16	AAR74432	Parathyroid hormon
947	11	37.9	35	16	AAR74433	Parathyroid hormon
948	11	37.9	35	16	AAR74434	Parathyroid hormon
949	11	37.9	35	16	AAR74435	Parathyroid hormon
950	11	37.9	35	16	AAR74436	Parathyroid hormon
951	11	37.9	35	16	AAR74437	Parathyroid hormon
952	11	37.9	35	16	AAR74438	Parathyroid hormon
953	11	37.9	35	16	AAR74439	Parathyroid hormon
954	11	37.9	35	16	AAR74440	Parathyroid hormon
955	11	37.9	35	16	AAR74441	Parathyroid hormon
956	11	37.9	35	16	AAR74442	Parathyroid hormon
957	11	37.9	35	16	AAR74443	Parathyroid hormon
958	11	37.9	35	16	AAR74444	Parathyroid hormon
959	11	37.9	35	16	AAR74445	Parathyroid hormon
960	11	37.9	35	16	AAR74446	Parathyroid hormon
961	11	37.9	35	16	AAR74447	Parathyroid hormon
962	11	37.9	35	16	AAR74423	Parathyroid hormon

963	11	37.9	35	16	AAR74429	Parathyroid hormon
964	11	37.9	35	16	AAR74430	Parathyroid hormon
965	11	37.9	35	16	AAR74431	Parathyroid hormon
966	11	37.9	35	16	AAR74398	Parathyroid hormon
967	11	37.9	35	16	AAR74399	Parathyroid hormon
968	11	37.9	35	16	AAR74400	Parathyroid hormon
969	11	37.9	35	16	AAR74406	Parathyroid hormon
970	11	37.9	35	16	AAR74407	Parathyroid hormon
971	11	37.9	35	16	AAR74408	Parathyroid hormon
972	11	37.9	35	16	AAR74409	Parathyroid hormon
973	11	37.9	35	16	AAR74394	Parathyroid hormon
974	11	37.9	35	16	AAR74395	Parathyroid hormon
975	11	37.9	35	16	AAR74396	Parathyroid hormon
976	11	37.9	35	16	AAR74397	Parathyroid hormon
977	11	37.9	36	12	AAR14729	Human parathyroid
978	11	37.9	36	15	AAR58042	[L8,D10,K11,L18] -h
979	11	37.9	36	15	AAR58044	[L8,D10,K11,A17,L1
980	11	37.9	36	15	AAR58055	[L8,Q18] -hPTH(1-36
981	11	37.9	36	15	AAR58057	[L8,D10,A16,Q18] -h
982	11	37.9	36	15	AAR55820	[L8,D10,K11,Q18] -h
983	11	37.9	36	15	AAR55824	[L8,D10,K11,A16,Q1
984	11	37.9	36	15	AAR58027	[A1,A3,L8,Q18] -hPT
985	11	37.9	36	15	AAR58031	[L8,K11,Q18] -hPTH(
986	11	37.9	36	15	AAR58072	Isopropyl- [L8,D10,
987	11	37.9	36	15	AAR58074	[L8,Y18] -hPTH(1-36
988	10	34.5	30	22	AAB84834	Parathyroid hormon
989	10	34.5	30	22	AAB96905	Parathyroid hormon
990	10	34.5	31	20	AAV02585	Parathyroid hormon
991	10	34.5	32	22	AAB84835	Parathyroid hormon
992	10	34.5	32	22	AAB96906	Parathyroid hormon
993	10	34.5	34	11	AAR08298	Rat parathyroid ho
994	10	34.5	34	11	AAR08301	Rat parathyroid ho
995	10	34.5	34	14	AAR41548	Modified hPTH (1-3
996	10	34.5	34	15	AAR58040	[L8,Q18,A29,E30,I3
997	10	34.5	34	15	AAR58045	[L8,Q16,D17,L18,R1
998	10	34.5	34	15	AAR58049	[L8,D10,K11,Q16,D1
999	10	34.5	34	15	AAR58056	[L8,D10,K11,A16,Q1
1000	10	34.5	34	15	AAR58058	[L8,D10,K11,A16,Q1

ALIGNMENTS

RESULT 1

AAR88836

ID AAR88836 standard; peptide; 29 AA.

XX

AC AAR88836;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-29)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 29
 FT /note= "amidated"
 XX
 PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILLICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 1; Fig 9; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 29 AA;

Query Match 100.0%; Score 29; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.6e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 2

AAU73063

ID AAU73063 standard; Peptide; 29 AA.

XX

AC AAU73063;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #45.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 29 AA;

Query Match 100.0%; Score 29; DB 23; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.6e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 3

AAR88832

ID AAR88832 standard; peptide; 30 AA.

XX

AC AAR88832;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-30)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 30

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 1; Fig 5; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density

CC without undesirable effects. They are useful for the treatment of

CC osteoporosis and other bone related disorders and disorders

CC involving bone cell calcium regulation.

XX

SQ Sequence 30 AA;

Query Match 100.0%; Score 29; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 4

AAU73051

ID AAU73051 standard; Peptide; 30 AA.

XX

AC AAU73051;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #33.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such

CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 30 AA;

Query Match 100.0%; Score 29; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 5

AAU73178

ID AAU73178 standard; Peptide; 30 AA.

XX

AC AAU73178;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #160.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.
PR 06-FEB-2001; 2001US-266673P.
PR 26-APR-2001; 2001US-0843221.

(AMGE-) AMGEN INC.

WPI; 2002-066435/09.

Disclosure; Page 63; 107pp; English.

The invention relates to a composition (I) comprising modulators of parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP) which comprise a PTH/PTHrP modulating domain and a vehicle. (I) comprising PTH agonist optionally with a bone resorption inhibitor, such as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates, oestrogens, oestrogen receptor modulators and tibolone is useful for treating osteopenia. (I) is useful for therapeutic and prophylactic purposes. Antagonists of PTH receptor are useful in treating primary and secondary hyperthyroidism, hypercalcaemia, tumour metastases, particularly breast and prostate cancer, cachexia and anorexia, osteopenia, including various forms of osteoporosis, Paget's disease of bone, osteomyelitis, osteonecrosis or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid arthritis, periodontal disease and alopecia. PTH receptor agonists are useful as therapeutic agents in conditions including fracture repair (including healing of non-union fractures), osteopenia, including various forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone and parathyroid hormone related protein (PTH/PTHrP) modulators and related amino acid sequences of the invention.

SQ Sequence 30 AA;

Query Match 100.0%; Score 29; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 2 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 30

RESULT 6

AAW42059

XX

XX

XX

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
 KW hypotensive action; bone.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 22
 FT /note= "Glu is bound to Lys at position 26 to form
 FT a cyclic structure"
 FT Modified-site 26
 FT /note= "Lys is bound to Glu at position 22 to form
 FT a cyclic structure"
 FT Modified-site 31
 FT /note= "amidated"
 XX
 PN WO9805683-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-CA00547.
 XX
 PR 14-MAR-1997; 97US-0040560.
 PR 02-AUG-1996; 96US-0691647.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
 PI Willick GE;
 XX
 DR WPI; 1998-145550/13.
 XX
 PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
 PT - for treating osteoporosis and fractures, also method for screening
 PT osteogenic peptide(s) based on their hypotensive action
 XX
 PS Claim 41; Fig 21; 77pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (hPTH)
 CC (1-31) peptide analogue. The present invention also describes a method
 CC for screening peptides for osteogenic activity by subcutaneous injection
 CC of a test compound and seeing if a small drop in arterial pressure
 CC occurs after a short time. The hPTH peptide analogue can be useful for
 CC stimulating bone growth, restoring bone and promoting bone healing,
 CC especially treatment of osteoporosis and normal fractures. The hPTH
 CC peptide analogue can be administered by injection or inhalation,
 CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
 CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
 CC the hormone and increases adenylyl cyclase (AC) activity, while
 CC cyclisation increases stability against proteases. The screening method,
 CC which can be performed in intact female animals, is a quick and simple
 CC way of identifying inactive compounds, avoiding the need for long-term,
 CC expensive tests on ovariectomised animals.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 19; Length 31;

Best Local Similarity 100.0%; Pred. No. 5.9e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 7

AAW42051

ID AAW42051 standard; peptide; 31 AA.

XX

AC AAW42051;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:6.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;

KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 27

FT /note= "Lys is bound to Asp at position 30 to form
a cyclic structure"

FT Modified-site 30

FT /note= "Asp is bound to Lys at position 27 to form
a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution

PT - for treating osteoporosis and fractures, also method for screening

PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 33; Fig 10; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)

CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenyllyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 8

AAAY02578

ID AAY02578 standard; peptide; 31 AA.

XX

AC AAY02578;

XX

DT 16-JUL-1999 (first entry)

XX

DE N-terminal 31 residues of human parathyroid hormone (hPTH).

XX

KW Human parathyroid hormone; hPTH; bone mass;

KW 3-(substituted phenoxy)benzo(b)thiophene compound;

KW bone loss treatment; osteoporosis.

XX

OS Homo sapiens.

XX

PN WO9918945-A1.

XX

PD 22-APR-1999.

XX

PF 05-OCT-1998; 98WO-US20848.

XX

PR 14-OCT-1997; 97US-0061800.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Sato M;

XX

DR WPI; 1999-287871/24.

XX

PT Method of building bone mass by co-administration of a parathyroid

PT hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound
XX
PS Claim 6; Page 39; 48pp; English.
XX
CC The present sequence represents a fragment of human parathyroid hormone
CC (hPTH). hPTH and its fragments are used in the method of the invention.
CC The specification describes a method for building bone mass, comprising
CC coadministration of a parathyroid hormone with a 3-(substituted
CC phenoxy)benzo(b)thiophene compound. The method is used for treatment
CC of bone loss, e.g. in osteoporosis.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 9

AAB81080

ID AAB81080 standard; peptide; 31 AA.

XX

AC AAB81080;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human parathyroid hormone 1-31.

XX

KW Parathyroid hormone; PTH; blood calcium level regulator; osteopathic;

KW vulnerary; bone growth; bone healing; osteoporosis; fracture; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 31

FT /note= "C-terminal amide"

XX

PN WO200121643-A2.

XX

PD 29-MAR-2001.

XX

PF 21-SEP-2000; 2000WO-CA01083.

XX

PR 22-SEP-1999; 99US-0406813.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Whitfield J, Willick GE;

XX

DR WPI; 2001-308081/32.

XX

PT New human parathyroid hormone (HPTH) analog useful for stimulating bone
PT growth, for restoring bone, for promotion of bone healing, and for

PT treating osteoporosis and normal fractures -
XX
PS Disclosure; Fig 2; 34pp; English.
XX
CC Parathyroid hormone (PTH) is a major regulator of blood calcium levels,
CC this invention relates to hPTH analogues, or their salts. Use of the
CC analogues results in osteopathic and vulnerary activity. The hPTH
CC analogues are useful for treating a warm-blooded animal for stimulating
CC bone growth, for restoring bone, and for the promotion of bone healing
CC during the treatment of osteoporosis and normal fractures. The present
CC sequence represents human parathyroid hormone hPTH-NH2.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 10

AAB91097

ID AAB91097 standard; Peptide; 31 AA.

XX
AC AAB91097;
XX
DT 22-JUN-2001 (first entry)
XX
DE Parathyroid hormone (PTH) related peptide SEQ ID NO:271.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents

XX
PA (HOLI/) HOLICK M F.
XX
PI Holick MF;
XX
DR WPI; 2002-452304/48.
DR N-PSDB; AAD37995.
XX
PT Regulating mammalian skin or hair cell proliferation and
PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -
XX
PS Disclosure; Fig 8; 56pp; English.
XX
CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 12

AAU73039

ID AAU73039 standard; Peptide; 31 AA.

XX

AC AAU73039;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #21.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 26; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.9e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||

Db

1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 13

AAU73177

ID AAU73177 standard; Peptide; 31 AA.

XX

AC AAU73177;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #159.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,

osteopenia, including various forms of osteoporosis, Paget's disease of bone, osteomyelitis, osteonecrosis or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid arthritis, periodontal disease and alopecia. PTH receptor agonists are useful as therapeutic agents in conditions including fracture repair (including healing of non-union fractures), osteopenia, including various forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone and parathyroid hormone related protein (PTH/PTHrP) modulators and related amino acid sequences of the invention.

SQ Sequence 31 AA;

Query Match 100.0%; Score 29; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity	100.0%;	Pred. No. 5.9e-22;
-----------------------	---------	--------------------

Best Local Similarity 100.0%; Pct. Ref. 9.98 12;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

[illegible]

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 14

AAU73176

ID AAU73176 standard; Peptide; 32 AA.

XX

AC AAU73176;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #158.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000: 2000US-214860P.

PR 06-FEB-2001: 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 32 AA;

Query Match 100.0%; Score 29; DB 23; Length 32;

Best Local Similarity 100.0%; Pred. No. 6.1e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 15

AAAY98018

ID AAY98018 standard; peptide; 33 AA.

XX

AC AAY98018;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human amino-terminal modified parathyroid hormone analogue # 9.

XX

KW Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;

KW signal transduction; osteoporosis; amino-terminal modification;

KW bone disease; parathyroid hormone receptor; osteopaenia;

KW hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.

XX

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Ser is desamino residue"
 XX
 PN WO200031137-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-US27656.
 XX
 PR 25-NOV-1998; 98US-0110152.
 XX
 PA (BRIN/) BRINGHURST F R.
 PA (TAKA/) TAKASU H.
 PA (GARD/) GARDELLA T J.
 XX
 PI Bringhurst FR, Takasu H, Gardella TJ;
 XX
 DR WPI; 2000-400045/34.
 XX
 PT New parathyroid hormone (PTH) analogs having one or more amino acid
 PT substitutions that confer PTH-1/PTH-2 receptor agonist properties,
 PT useful for treating old age osteoporosis and post-menopausal
 PT osteoporosis -
 XX
 PS Disclosure; Page 65; 69pp; English.
 XX
 CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
 CC cells, initiating signal transduction. It has been identified that the
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the
 CC amino terminal is important for signal transduction. The present
 CC sequence is a human PTH peptide, with an amino-terminal modification
 CC which results in effective activation of the PTH-2 receptor and therefore
 CC downstream signalling. Aberrant PTH activity has been implicated in a
 CC number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. This
 CC peptide would be suitable for prophylaxis and treatment of the above
 CC disorders. In addition, the present sequence would be suitable for
 CC fracture repair. The present sequence is modified to have a
 CC desamino residue at position 1.
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 29; DB 21; Length 33;
 Best Local Similarity 100.0%; Pred. No. 6.2e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

ID AAP30022 standard; peptide; 34 AA.
 XX
 AC AAP30022;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-SEP-1992 (first entry)
 XX
 DE Human parathyroid-(1-34) amide.
 XX
 KW PTH; parathyroid gland; antibodies.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 34
 FT /note= "amidated"
 XX
 PN JP58096052-A.
 XX
 PD 07-JUN-1983.
 XX
 PF 30-NOV-1983; 83JP-0193212.
 XX
 PR 31-MAR-1981; 81JP-0048887.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1983-709291/28.
 XX
 PT High activity human parathyroid hormone amide prodn. - by
 PT condensing protected aminoacid(s) and/or peptide(s) useful for
 PT lowering parathyroid gland function
 XX
 PS Claim 1; Page 1; 20pp; Japanese.
 XX
 CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNIGKHLNSMERVEWLRKKLQ 29
 ||||||||||||||||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 17

AAP50377

ID AAP50377 standard; peptide; 34 AA.

XX

AC AAP50377;

XX

DT 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX

DE [Met(O)8,18]hPTH-(1-34).

XX

KW Human parathyroid hormone; calcium regulation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 8

FT /label= oxidised methionine

FT Modified-site 18

FT /label= oxidised methionine

XX

PN JP59204159-A.

XX

PD 19-NOV-1984.

XX

PF 28-APR-1983; 83JP-0075607.

XX

PR 28-APR-1983; 83JP-0075607.

XX

PA (TOXN) TOYO JOZO KK.

XX

DR WPI; 1985-003560/01.

XX

PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in

PT blood and decreases level in urine.

XX

PS Claim 1; Page 1; 3pp; Japanese.

XX

CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,

CC decreases Ca in urine and increases P in urine by increasing cAMP in

CC urine and enhancing vitamin D hydroxylase activity in kidneys. The

CC modified derivative only has the effect of lowering Ca levels in

CC urine and can be used when only this particular effect is required.

CC (Updated on 25-MAR-2003 to correct PA field.)

CC (Updated on 25-MAR-2003 to correct DR field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

||||||||||||||||||||||||||||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 18

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone
DE obtainable from a human or animal.

XX

KW Osteoporosis therapy.

XX

OS Homo sapiens/animal.

XX

PN EP197514-A.

XX

PD 15-OCT-1986.

XX

PF 03-APR-1986; 86EP-0104562.

XX

PR 04-APR-1985; 85US-0720018.

PR 05-DEC-1986; 86US-0939308.

PR 21-MAY-1987; 87US-0052383.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Potts JT, Neer RM, Slovik DM;

XX

DR WPI; 1986-273437/42.

XX

PT Compsn. and kits for increasing bone mass in osteoporosis -

PT contg. parathyroid hormone or fragment with hydroxylated

PT vitamin/D cpd. or calcium salt

XX

PS Claim 4; Page 24; 26pp; English.

XX

CC The peptide is used in a pharmaceutical compsn. together with a
CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 7; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 19

AAR07919

ID AAR07919 standard; protein; 34 AA.

XX

AC AAR07919;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN US4968669-A.

XX

PD 06-NOV-1990.

XX

PF 21-APR-1989; 89US-0341597.

XX

PR 21-APR-1989; 89US-0341597.

PR 09-MAY-1988; 88US-0191512.

XX

PA (MERI) MERCK & CO INC.

XX

PI Rosenblatt M, Chorev M;

XX

DR WPI; 1990-354642/47.

XX

PT New para:thyroid hormone analogues - which inhibit hormone

PT activity by binding receptors while not producing second

PT messenger molecules

XX

PS Claim 1; Column 8; 6pp; English.

XX

CC Peptide analogues have high affinity for PTH cell surface receptors,

CC but do not stimulate production of secondary messenger molecules.

CC They may be used in inhibition of PTH action, and in diagnosis and

CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.

CC Analogues may also be used in treatment of tumours and other cells

CC overproducing peptide hormone-like substances, and immune diseases

CC eg. allergic inflammation and hyperactive lymphocytes.

CC Naturally occurring PTH levels may also be measured in vitro.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 11; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 20

AAR07922

ID AAR07922 standard; protein; 34 AA.

XX

AC AAR07922;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, Tyr34 hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN US4968669-A.

XX

PD 06-NOV-1990.

XX

PF 21-APR-1989; 89US-0341597.

XX

PR 21-APR-1989; 89US-0341597.

PR 09-MAY-1988; 88US-0191512.

XX

PA (MERI) MERCK & CO INC.

XX

PI Rosenblatt M, Chorev M;

XX

DR WPI; 1990-354642/47.

XX

PT New para:thyroid hormone analogues - which inhibit hormone

PT activity by binding receptors while not producing second

PT messenger molecules

XX

PS Claim 1; Column 8; 6pp; English.

XX

CC Peptide analogues have high affinity for PTH cell surface receptors,
CC but do not stimulate production of secondary messenger molecules.

CC They may be used in inhibition of PTH action, and in diagnosis and
CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.

CC Analogues may also be used in treatment of tumours and other cells
CC overproducing peptide hormone-like substances, and immune diseases

CC eg. allergic inflammation and hyperactive lymphocytes.

CC Naturally occurring PTH levels may also be measured in vitro.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 11; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 21

AAR22283

ID AAR22283 standard; peptide; 34 AA.
 XX
 AC AAR22283;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 XX
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX
 OS Homo sapiens.
 XX
 PN WO9204039-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Holick MF;
 XX
 DR WPI; 1992-114063/14.
 XX
 PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;

 Query Match 100.0%; Score 29; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

AAR41549

ID AAR41549 standard; protein; 34 AA.

XX

AC AAR41549;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ser3]hPTH (1-34)NH2.

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;

KW hypoparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 3

FT /note = "D-form residue"

FT Modified-site 34

FT /note = "C terminal is amidated"

XX

PN EP561412-A1.

XX

PD 22-SEP-1993.

XX

PF 18-MAR-1993; 93EP-0104500.

XX

PR 19-MAR-1992; 92JP-0063517.

PR 18-FEB-1993; 93JP-0029283.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Nakagawa S, Taketomi S;

XX

DR WPI; 1993-296712/38.

XX

PT New parathyroid hormone derivs. - used for the treatment of

PT osteoporosis hypoparathyroidism and hypertension

XX

PS Example 1; Page 17; 37pp; English.

XX

CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;

CC AAR41549-R41582 - specific examples) show increased resistance to

CC proteases and a greater persistency of activity within the blood is

CC obtained. The proteins can be used to treat a number of bone and blood

CC disorders. This analogue was used as a test compound.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 14; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 23

AAR41570

ID AAR41570 standard; protein; 34 AA.

XX

AC AAR41570;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [Gln25]hPTH (1-34).

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;

KW hypoparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN EP561412-A1.

XX

PD 22-SEP-1993.

XX

PF 18-MAR-1993; 93EP-0104500.

XX

PR 19-MAR-1992; 92JP-0063517.

PR 18-FEB-1993; 93JP-0029283.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Nakagawa S, Taketomi S;

XX

DR WPI; 1993-296712/38.

XX

PT New parathyroid hormone derivs. - used for the treatment of

PT osteoporosis hypoparathyroidism and hypertension

XX

PS Example 1; Page 27; 37pp; English.

XX

CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;

CC AAR41549-R41582 - specific examples) show increased resistance to

CC proteases and a greater persistency of activity within the blood is

CC obtained. The proteins can be used to treat a number of bone and blood

CC disorders. This analogue was used as a test compound.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 14; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 24

AAR58291

ID AAR58291 standard; peptide; 34 AA.

XX

AC AAR58291;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys (For) 26, Lys (For) 27] -hPTH(1-34) -NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 26

FT /label= Other

FT /note= "Formyl-Lys."

FT Modified-site 27

FT /label= Other

FT /note= "Formyl-Lys."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 289; Page 47; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering

XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 226; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 26

AAR58232

ID AAR58232 standard; peptide; 34 AA.
 XX
 AC AAR58232;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys32]-hPTH(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 230; Page 45; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 27

AAR58181

ID AAR58181 standard; peptide; 34 AA.

XX

AC AAR58181;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Thr33, Ala34]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 179; Page 43; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 28

AAR58016

ID AAR58016 standard; peptide; 34 AA.

XX

AC AAR58016;

XX

DT 20-SEP-1994 (first entry)
 XX
 DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-alpha-isopropyl-Ser"
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 29

AAR58017

ID AAR58017 standard; peptide; 34 AA.

XX

AC AAR58017;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys (N-epsilon-Isopropyl) 26,27] -human parathyroid hormone (1-34) -NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 26

FT /note= "N-epsilon-Isopropyl-Lys"

FT Modified-site 27

FT /note= "N-epsilon-Isopropyl-Lys"

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
XX
PS Example 2; Page 32; 92pp; English.
XX
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 30

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;

KW antiproliferative; tumor; psoriasis; docosaheptaenoic acid; DHA;

KW eicosapentaenoic acid; EPA; antitumor.

XX

OS Synthetic.

XX

PN WO9412530-A1.

XX

PD 09-JUN-1994.

XX

PF 29-NOV-1993; 93WO-HU00065.

XX

PR 30-NOV-1992; 92US-0984293.

XX

PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.

PA (SYNT-) SYNTHETIC PEPTIDES INC.

XX

PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;

PI Szederkenyi F, Vadasz Z;

XX

DR WPI; 1994-200194/24.

XX

PT New fatty acyl-peptide conjugates for inhibiting cell

PT proliferation - more active than free peptide, partic. for

PT treating tumours, virus-infected cells, psoriasis, etc.
XX
PS Disclosure; Fig. 1; 45pp; English.
XX
CC The peptides given in AAR55718-48 can each be conjugated through an
CC amide linkage with a polyunsaturated fatty acid moiety, such as
CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve
CC antiproliferative activity. The parathormone N-terminal fragment
CC inhibits osteoblast proliferation.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 31

AAR74521

ID AAR74521 standard; Peptide; 34 AA.

XX

AC AAR74521;

XX

DT 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX

DE Human parathyroid hormone (1-34).

XX

KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;

KW osteoporosis; hypercalcaemia; hyperparathroidism;

KW metabolic bone disease; human; veterinary medicine;

KW iontophoretic transdermal transport; recombinant E.coli.

XX

OS Homo sapiens.

XX

PN WO9511988-A1.

XX

PD 04-MAY-1995.

XX

PF 25-OCT-1994; 94WO-US12205.

XX

PR 25-OCT-1993; 93US-0142551.

XX

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX

PI Oldenburg KR, Selick HE;

XX

DR WPI; 1995-178880/23.

XX

PT New active analogues of parathyroid hormone - with increased

PT activity, stability in serum etc., esp. for treating

PT osteoporosis, also related DNA and vectors

XX
 PS Disclosure; Page 1; 109pp; English.
 XX
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (RPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 32

AAW99449

ID AAW99449 standard; peptide; 34 AA.

XX

AC AAW99449;

XX

DT 08-JUN-1999 (first entry)

XX

DE Human parathyroid hormone aa1-34.

XX

KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
 KW spontaneous abortion; uterine contraction; human.

XX

OS Homo sapiens.

XX

PN US5880093-A.

XX

PD 09-MAR-1999.

XX

PF 05-APR-1995; 95US-0411726.

XX

PR 28-SEP-1992; 92IT-MI02331.

XX

PA (BAGN/) BAGNOLI F.

XX

PI Bagnoli F;

XX

DR WPI; 1996-162392/17.

XX

PT Use of composition containing parathormone or fragments - for
PT preventing premature birth or spontaneous abortion or for treating
PT unwanted uterine contractions
XX
PS Disclosure; Column 7-8; 11pp; English.
XX
CC Peptides AAW99448-W99452 represent all or part of the parathyroid
CC hormone (PTH; parathormone) sequence or related peptide. The peptides
CC are used for preventing premature birth, spontaneous abortion or unwanted
CC uterine contractions in a pregnant human patient.
CC (Note: this patent is the first Major Country Equivalent to Italian
CC Patent IT1255388).
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 33

AAR99978

ID AAR99978 standard; peptide; 34 AA.
XX
AC AAR99978;
XX
DT 30-APR-1997 (first entry)
XX
DE Human parathyroid hormone peptide fragment (1-34).
XX
KW cyclic parathyroid hormone fragment; calcium-regulating activity;
KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
KW improved half life; calcium retention; bone.
XX
OS Synthetic.
XX
PN DE19508672-A1.
XX
PD 12-SEP-1996.
XX
PF 10-MAR-1995; 95DE-1008672.
XX
PR 10-MAR-1995; 95DE-1008672.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
XX
PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
XX
DR WPI; 1996-413519/42.
XX
PT Cyclic parathyroid hormone fragments with lactam bridge - have good
PT in vivo half life and are useful for treating osteoporosis and
PT preventing epidermal cell proliferation

XX
 PS Disclosure; Page 9; 14pp; German.
 XX
 CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
 CC sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
 CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
 CC the N-terminus, and are cyclised between positions 13 and 17. One of
 CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
 CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
 CC treating osteoporosis and inhibit proliferation of epidermal cells (for
 CC treating psoriasis). The CPTH have an improved half life in vivo than
 CC known PTH fragments, increased mitogenicity and DNA-synthesising
 CC capacity, reduced catabolic, calcium-mobilising activity and increased
 CC activity for calcium retention and incorporation into bone. The
 CC present sequence is that of human PTH peptide fragment (1-34).
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 34

AAR98951

ID AAR98951 standard; peptide; 34 AA.
 XX
 AC AAR98951;
 XX
 DT 15-JAN-1997 (first entry)
 XX
 DE Target peptide (PTH(1-34)) used in fusion protein construct.
 XX
 KW Fusion protein construct; isolation; purification;
 KW growth hormone releasing factor; glucagon-like peptide 1;
 KW parathyroid hormone; inclusion body; carbonic anhydrase.
 XX
 OS Synthetic.
 XX
 PN WO9617942-A1.
 XX
 PD 13-JUN-1996.
 XX
 PF 07-DEC-1995; 95WO-US15800.
 XX
 PR 07-DEC-1994; 94US-0350530.
 XX
 PA (BION-) BIONEBRASKA INC.
 XX
 PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;
 PI Partridge BE, Stout JS, Wagner FW;
 XX
 DR WPI; 1996-287186/29.

XX
PT Isolation and purificn of peptide(s) from fusion protein constructs
PT - which include a carbonic anhydrase and a variable fused
PT polypeptide

XX
PS Claim 18; Page 48; 67pp; English.

XX
CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a
CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-34 of PTH.

XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 35

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;

KW fusion protein; transpeptidation.

XX

OS Not specified.

XX

PN W09617941-A2.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15799.

XX

PR 07-DEC-1994; 94US-0350528.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;

PI Wagner FW;

XX
 DR WPI; 1996-287185/29.
 XX
 PT Production of C-terminal alpha-carboxamidated peptide(s) - by
 PT cleavage and transpeptidation of recombinant multicopy peptide(s) or
 PT fusion constructs
 XX
 PS Claim 12; Page 70; 93pp; English.
 XX
 CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be
 CC produced as C-terminal amidated peptides utilising novel recombinant
 CC protein constructs (see also AAR98967-72) in which single or multiple
 CC copies of the peptide are linked by intraconnecting peptides that
 CC permit the construct to be selectively reacted to produce product
 CC peptides having a C-terminal alpha-carboxamide. Expression cassettes
 CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.
 CC of the recombinant proteins in transformed E. coli host cells.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 36

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX

AC AAR88835;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
 KW calcium regulation; reduced PKC activity; protein kinase C;
 KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10
 FT /note= "forms peptide bond with Lys at posn. 26"
 FT Modified-site 14
 FT /note= "forms peptide bond with Asp at posn. 30"
 FT Modified-site 26
 FT /note= "forms peptide bond with Asn at posn. 10"
 FT Modified-site 30
 FT /note= "forms peptide bond with His at posn. 14"
 FT Modified-site 34
 FT /note= "amidated"

XX

PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILLICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 3; Fig 8; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 37

AAW24273

ID AAW24273 standard; protein; 34 AA.
 XX
 AC AAW24273;
 XX
 DT 17-OCT-1997 (first entry)
 XX
 DE Wild type parathyroid hormone.
 XX
 KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;
 KW electrotransportability; alpha-helix; beta-sheet.
 XX
 OS Homo sapiens.
 XX
 PN W09639423-A2.
 XX
 PD 12-DEC-1996.

XX
 PF 06-JUN-1996; 96WO-US09647.
 XX
 PR 06-JUN-1995; 95US-0468275.
 XX
 PA (ALZA) ALZA CORP.
 XX
 PI Holladay LA, Oldenburg KR;
 XX
 DR WPI; 1997-043058/04.
 XX
 PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid
 PT hormone and hirulog - which exhibit better or enhanced
 PT electro-transportability through a body surface
 XX
 PS Claim 7; Fig 1A; 55pp; English.
 XX
 CC The sequences given in AAW24273-76 represent wildtype and analogues of
 CC parathyroid hormone (PTH). The analogues exhibit better/enhanced
 CC electrotransportability through a body surface, and are characterised
 CC by substituting one or more amino acid residues of the parent
 CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet
 CC segments of the parent polypeptide. An electrotransport device can
 CC deliver the polypeptide analogue through a body surface by electro-
 CC transport by including providing a therapeutically effective amount
 CC of the polypeptide analogue in a donor reservoir of the electrotransport
 CC device. The electrotransport flux of a polypeptide is increased by
 CC reducing the potential of the polypeptide for forming alpha-helix or
 CC beta-sheet segment.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 38

AAW19994

ID AAW19994 standard; peptide; 34 AA.

XX

AC AAW19994;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;

KW adenylate cyclase activity; bone growth; osteoporosis; fracture;

KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT Misc-difference 13
 FT /note= "joined via amide bond to residue 17"
 FT Misc-difference 17
 FT /note= "joined via amide bond to residue 13"
 FT Misc-difference 34
 FT /note= "amidated"
 XX
 PN WO9640193-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09674.
 XX
 PR 07-JUN-1995; 95US-0488105.
 XX
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 XX
 PI Chorev M, Rosenblatt M;
 XX
 DR WPI; 1997-051884/05.
 XX
 PT New cyclic analogues of parathyroid hormone - having di:sulphide or
 PT amide bond between residues 13 and 17 and/or between residues 26 and
 PT 30, useful for treating osteoporosis and bone fractures
 XX
 PS Claim 4; Page -; 23pp; English.
 XX
 CC AAW19994 is a cyclised peptide derived from the N-terminal sequence
 CC of human parathyroid hormone (PTH). The peptide is able to bind to
 CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
 CC PTH peptides stimulate bone growth and thus are useful in the
 CC treatment of osteoporosis and bone fractures. Optionally they may
 CC be administered concurrently with antiresorptive therapy (e.g.
 CC bisphosphonate and calcitonin).
 CC N.B. sequence not given in the specification, created from known
 CC sequence of amino acids 1-34 of human PTH.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 39
 AAW20000
 ID AAW20000 standard; peptide; 34 AA.
 XX
 AC AAW20000;
 XX
 DT 28-AUG-1997 (first entry)
 XX

DE Cyclised human parathyroid hormone (1-34) amide.
 XX
 KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
 KW adenylate cyclase activity; bone growth; osteoporosis; fracture;
 KW antiresorptive therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 26
 FT /note= "joined via amide bond to residue 30"
 FT Misc-difference 30
 FT /note= "joined via amide bond to residue 26"
 FT Misc-difference 34
 FT /note= "amidated"
 XX
 PN WO9640193-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09674.
 XX
 PR 07-JUN-1995; 95US-0488105.
 XX
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 XX
 PI Chorev M, Rosenblatt M;
 XX
 DR WPI; 1997-051884/05.
 XX
 PT New cyclic analogues of parathyroid hormone - having di:sulphide or
 PT amide bond between residues 13 and 17 and/or between residues 26 and
 PT 30, useful for treating osteoporosis and bone fractures
 XX
 PS Claim 6; Page -; 23pp; English.
 XX
 CC AAW20000 is a cyclised peptide derived from the N-terminal sequence
 CC of human parathyroid hormone (PTH). The peptide is able to bind to
 CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
 CC PTH peptides stimulate bone growth and thus are useful in the
 CC treatment of osteoporosis and bone fractures. Optionally they may
 CC be administered concurrently with antiresorptive therapy (e.g.
 CC bisphosphonate and calcitonin).
 CC N.B. sequence not given in the specification, created from known
 CC sequence of amino acids 1-34 of human PTH.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 40

AAW20006

ID AAW20006 standard; peptide; 34 AA.

XX

AC AAW20006;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;

KW adenylate cyclase activity; bone growth; osteoporosis; fracture;

KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 26

FT /note= "joined via amide bond to residue 30"

FT Misc-difference 30

FT /note= "joined via amide bond to residue 26"

FT Misc-difference 34

FT /note= "amidated"

XX

PN WO9640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.

XX

PR 07-JUN-1995; 95US-0488105.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PI Chorev M, Rosenblatt M;

XX

DR WPI; 1997-051884/05.

XX

PT New cyclic analogues of parathyroid hormone - having di:sulphide or
PT amide bond between residues 13 and 17 and/or between residues 26 and
PT 30, useful for treating osteoporosis and bone fractures

XX

PS Claim 8; Page -; 23pp; English.

XX

CC AAW20006 is a cyclised peptide derived from the N-terminal sequence
CC of human parathyroid hormone (PTH). The peptide is able to bind to
CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
CC PTH peptides stimulate bone growth and thus are useful in the
CC treatment of osteoporosis and bone fractures. Optionally they may
CC be administered concurrently with antiresorptive therapy (e.g.
CC bisphosphonate and calcitonin).

CC N.B. sequence not given in the specification, created from known
CC sequence of amino acids 1-34 of human PTH.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 29; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Search completed: January 14, 2004, 10:34:27
Job time : 28.7352 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 9.84735 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-167
Perfect score: 29
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	29	100.0	30	1	US-08-262-495C-5	Sequence 5, Appli
2	29	100.0	31	1	US-08-262-495C-3	Sequence 3, Appli
3	29	100.0	31	2	US-08-691-647C-1	Sequence 1, Appli
4	29	100.0	31	2	US-08-691-647C-6	Sequence 6, Appli
5	29	100.0	31	3	US-08-904-760B-1	Sequence 1, Appli
6	29	100.0	31	3	US-08-904-760B-6	Sequence 6, Appli
7	29	100.0	31	3	US-08-904-760B-14	Sequence 14, Appli
8	29	100.0	31	3	US-08-904-760B-32	Sequence 32, Appli
9	29	100.0	31	4	US-09-406-813-2	Sequence 2, Appli
10	29	100.0	31	4	US-09-536-785A-1	Sequence 1, Appli
11	29	100.0	31	4	US-09-536-785A-6	Sequence 6, Appli

12	29	100.0	31	4	US-09-536-785A-14	Sequence 14, Appl
13	29	100.0	31	4	US-09-536-785A-32	Sequence 32, Appl
14	29	100.0	33	4	US-09-447-800-9	Sequence 9, Appli
15	29	100.0	34	1	US-07-765-373-1	Sequence 1, Appli
16	29	100.0	34	1	US-08-033-099-1	Sequence 1, Appli
17	29	100.0	34	1	US-08-262-495C-1	Sequence 1, Appli
18	29	100.0	34	1	US-07-915-247A-1	Sequence 1, Appli
19	29	100.0	34	1	US-08-443-863-1	Sequence 1, Appli
20	29	100.0	34	1	US-08-448-070-1	Sequence 1, Appli
21	29	100.0	34	1	US-08-488-105-7	Sequence 7, Appli
22	29	100.0	34	1	US-08-468-275-6	Sequence 6, Appli
23	29	100.0	34	1	US-08-449-500-1	Sequence 1, Appli
24	29	100.0	34	1	US-08-449-317A-1	Sequence 1, Appli
25	29	100.0	34	2	US-08-142-551B-2	Sequence 2, Appli
26	29	100.0	34	2	US-08-477-022-1	Sequence 1, Appli
27	29	100.0	34	2	US-08-449-447-1	Sequence 1, Appli
28	29	100.0	34	2	US-08-835-231-13	Sequence 13, Appl
29	29	100.0	34	2	US-08-184-328-1	Sequence 1, Appli
30	29	100.0	34	2	US-08-411-726-2	Sequence 2, Appli
31	29	100.0	34	2	US-08-691-647C-5	Sequence 5, Appli
32	29	100.0	34	2	US-08-521-097-1	Sequence 1, Appli
33	29	100.0	34	3	US-09-044-536A-1	Sequence 1, Appli
34	29	100.0	34	3	US-08-904-760B-22	Sequence 22, Appl
35	29	100.0	34	3	US-08-903-497A-1	Sequence 1, Appli
36	29	100.0	34	3	US-09-108-661-13	Sequence 13, Appl
37	29	100.0	34	4	US-09-007-466-6	Sequence 6, Appli
38	29	100.0	34	4	US-09-406-813-1	Sequence 1, Appli
39	29	100.0	34	4	US-08-952-980B-6	Sequence 6, Appli
40	29	100.0	34	4	US-09-635-076-1	Sequence 1, Appli
41	29	100.0	34	4	US-09-228-990-1	Sequence 1, Appli
42	29	100.0	34	4	US-09-447-800-8	Sequence 8, Appli
43	29	100.0	34	4	US-09-536-785A-22	Sequence 22, Appl
44	29	100.0	34	4	US-09-442-989-26	Sequence 26, Appl
45	29	100.0	34	5	PCT-US95-15800-22	Sequence 22, Appl
46	29	100.0	35	1	US-08-256-363-3	Sequence 3, Appli
47	29	100.0	36	1	US-08-256-363-4	Sequence 4, Appli
48	29	100.0	37	1	US-08-440-117-1	Sequence 1, Appli
49	29	100.0	37	3	US-09-068-738A-16	Sequence 16, Appl
50	29	100.0	38	1	US-08-112-024-1	Sequence 1, Appli
51	29	100.0	38	1	US-08-232-849-1	Sequence 1, Appli
52	29	100.0	38	2	US-08-625-586-1	Sequence 1, Appli
53	29	100.0	38	3	US-09-128-401-1	Sequence 1, Appli
54	28	96.6	28	4	US-09-448-867-12	Sequence 12, Appl
55	28	96.6	33	4	US-09-447-800-3	Sequence 3, Appli
56	28	96.6	33	4	US-09-447-800-6	Sequence 6, Appli
57	28	96.6	34	4	US-09-447-800-1	Sequence 1, Appli
58	28	96.6	34	4	US-09-447-800-2	Sequence 2, Appli
59	28	96.6	34	4	US-09-447-800-5	Sequence 5, Appli
60	28	96.6	36	1	US-08-112-024-2	Sequence 2, Appli
61	27	93.1	28	4	US-09-448-867-8	Sequence 8, Appli
62	27	93.1	28	4	US-09-448-867-10	Sequence 10, Appl
63	27	93.1	33	1	US-08-256-363-1	Sequence 1, Appli
64	27	93.1	34	1	US-08-256-363-2	Sequence 2, Appli
65	26	89.7	28	4	US-09-406-813-3	Sequence 3, Appli
66	26	89.7	29	4	US-09-406-813-4	Sequence 4, Appli
67	26	89.7	30	1	US-08-262-495C-6	Sequence 6, Appli
68	26	89.7	30	3	US-08-904-760B-7	Sequence 7, Appli

69	26	89.7	30	4	US-09-536-785A-7	Sequence 7, Appli
70	26	89.7	31	1	US-08-262-495C-4	Sequence 4, Appli
71	26	89.7	31	2	US-08-691-647C-2	Sequence 2, Appli
72	26	89.7	31	2	US-08-691-647C-3	Sequence 3, Appli
73	26	89.7	31	2	US-08-691-647C-4	Sequence 4, Appli
74	26	89.7	31	3	US-08-904-760B-2	Sequence 2, Appli
75	26	89.7	31	3	US-08-904-760B-3	Sequence 3, Appli
76	26	89.7	31	3	US-08-904-760B-4	Sequence 4, Appli
77	26	89.7	31	3	US-08-904-760B-5	Sequence 5, Appli
78	26	89.7	31	3	US-08-904-760B-8	Sequence 8, Appli
79	26	89.7	31	3	US-08-904-760B-11	Sequence 11, Appl
80	26	89.7	31	3	US-08-904-760B-12	Sequence 12, Appl
81	26	89.7	31	3	US-08-904-760B-15	Sequence 15, Appl
82	26	89.7	31	3	US-08-904-760B-16	Sequence 16, Appl
83	26	89.7	31	3	US-08-904-760B-17	Sequence 17, Appl
84	26	89.7	31	4	US-09-536-785A-2	Sequence 2, Appli
85	26	89.7	31	4	US-09-536-785A-3	Sequence 3, Appli
86	26	89.7	31	4	US-09-536-785A-4	Sequence 4, Appli
87	26	89.7	31	4	US-09-536-785A-5	Sequence 5, Appli
88	26	89.7	31	4	US-09-536-785A-8	Sequence 8, Appli
89	26	89.7	31	4	US-09-536-785A-11	Sequence 11, Appl
90	26	89.7	31	4	US-09-536-785A-12	Sequence 12, Appl
91	26	89.7	31	4	US-09-536-785A-15	Sequence 15, Appl
92	26	89.7	31	4	US-09-536-785A-16	Sequence 16, Appl
93	26	89.7	31	4	US-09-536-785A-17	Sequence 17, Appl
94	26	89.7	34	1	US-08-262-495C-2	Sequence 2, Appli
95	26	89.7	34	3	US-08-904-760B-9	Sequence 9, Appli
96	26	89.7	34	3	US-08-904-760B-10	Sequence 10, Appl
97	26	89.7	34	4	US-09-449-632-24	Sequence 24, Appl
98	26	89.7	34	4	US-09-536-785A-9	Sequence 9, Appli
99	26	89.7	34	4	US-09-536-785A-10	Sequence 10, Appl
100	25	86.2	31	3	US-08-904-760B-21	Sequence 21, Appl
101	25	86.2	31	4	US-09-536-785A-21	Sequence 21, Appl
102	24	82.8	34	1	US-07-773-098-5	Sequence 5, Appli
103	24	82.8	34	1	US-07-773-098-6	Sequence 6, Appli
104	23	79.3	38	5	PCT-US95-15800-29	Sequence 29, Appl
105	21	72.4	31	3	US-08-904-760B-18	Sequence 18, Appl
106	21	72.4	31	3	US-08-904-760B-19	Sequence 19, Appl
107	21	72.4	31	3	US-08-904-760B-20	Sequence 20, Appl
108	21	72.4	31	4	US-09-536-785A-18	Sequence 18, Appl
109	21	72.4	31	4	US-09-536-785A-19	Sequence 19, Appl
110	21	72.4	31	4	US-09-536-785A-20	Sequence 20, Appl
111	20	69.0	34	4	US-08-952-980B-9	Sequence 9, Appli
112	19	65.5	34	3	US-09-044-536A-9	Sequence 9, Appli
113	19	65.5	34	3	US-09-044-536A-10	Sequence 10, Appl
114	19	65.5	34	3	US-09-044-536A-13	Sequence 13, Appl
115	19	65.5	34	3	US-09-044-536A-14	Sequence 14, Appl
116	19	65.5	34	3	US-09-044-536A-15	Sequence 15, Appl
117	18	62.1	28	4	US-09-448-867-6	Sequence 6, Appli
118	18	62.1	34	3	US-09-044-536A-8	Sequence 8, Appli
119	18	62.1	34	3	US-09-044-536A-11	Sequence 11, Appl
120	18	62.1	34	3	US-09-044-536A-12	Sequence 12, Appl
121	17	58.6	28	4	US-09-448-867-1	Sequence 1, Appli
122	17	58.6	28	4	US-09-448-867-2	Sequence 2, Appli
123	17	58.6	28	4	US-09-448-867-4	Sequence 4, Appli
124	16	55.2	28	4	US-09-406-813-6	Sequence 6, Appli
125	16	55.2	31	4	US-09-406-813-5	Sequence 5, Appli

126	16	55.2	34	1	US-08-488-105-1	Sequence 1, Appli
127	16	55.2	34	1	US-08-488-105-13	Sequence 13, Appl
128	16	55.2	34	3	US-09-044-536A-26	Sequence 26, Appl
129	15	51.7	34	1	US-07-915-247A-3	Sequence 3, Appli
130	15	51.7	34	1	US-08-443-863-3	Sequence 3, Appli
131	15	51.7	34	1	US-08-448-070-3	Sequence 3, Appli
132	15	51.7	34	1	US-08-449-500-3	Sequence 3, Appli
133	15	51.7	34	1	US-08-449-317A-3	Sequence 3, Appli
134	15	51.7	34	2	US-08-477-022-3	Sequence 3, Appli
135	15	51.7	34	2	US-08-449-447-3	Sequence 3, Appli
136	15	51.7	34	2	US-08-184-328-3	Sequence 3, Appli
137	15	51.7	34	2	US-08-521-097-3	Sequence 3, Appli
138	15	51.7	34	3	US-09-044-536A-25	Sequence 25, Appl
139	15	51.7	34	3	US-09-044-536A-29	Sequence 29, Appl
140	15	51.7	34	3	US-08-903-497A-3	Sequence 3, Appli
141	15	51.7	34	4	US-09-635-076-3	Sequence 3, Appli
142	14	48.3	34	1	US-08-488-105-3	Sequence 3, Appli
143	14	48.3	34	1	US-08-488-105-9	Sequence 9, Appli
144	14	48.3	34	1	US-08-488-105-15	Sequence 15, Appl
145	14	48.3	34	3	US-08-903-497A-7	Sequence 7, Appli
146	14	48.3	34	4	US-09-635-076-7	Sequence 7, Appli
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149	13	44.8	30	3	US-08-904-760B-35	Sequence 35, Appl
150	13	44.8	30	4	US-09-536-785A-33	Sequence 33, Appl
151	13	44.8	30	4	US-09-536-785A-34	Sequence 34, Appl
152	13	44.8	30	4	US-09-536-785A-35	Sequence 35, Appl
153	13	44.8	34	1	US-07-915-247A-2	Sequence 2, Appli
154	13	44.8	34	1	US-08-443-863-2	Sequence 2, Appli
155	13	44.8	34	1	US-08-448-070-2	Sequence 2, Appli
156	13	44.8	34	1	US-08-488-105-2	Sequence 2, Appli
157	13	44.8	34	1	US-08-488-105-8	Sequence 8, Appli
158	13	44.8	34	1	US-08-449-500-2	Sequence 2, Appli
159	13	44.8	34	1	US-08-449-317A-2	Sequence 2, Appli
160	13	44.8	34	2	US-08-477-022-2	Sequence 2, Appli
161	13	44.8	34	2	US-08-449-447-2	Sequence 2, Appli
162	13	44.8	34	2	US-08-184-328-2	Sequence 2, Appli
163	13	44.8	34	2	US-08-521-097-2	Sequence 2, Appli
164	13	44.8	34	3	US-09-044-536A-18	Sequence 18, Appl
165	13	44.8	34	3	US-09-044-536A-19	Sequence 19, Appl
166	12	41.4	34	1	US-08-049-402-2	Sequence 2, Appli
167	12	41.4	34	1	US-08-488-105-14	Sequence 14, Appl
168	12	41.4	34	1	US-08-526-987-2	Sequence 2, Appli
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172	11	37.9	34	1	US-08-488-105-6	Sequence 6, Appli
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177	11	37.9	34	1	US-08-449-500-79	Sequence 79, Appl
178	11	37.9	34	1	US-08-449-317A-79	Sequence 79, Appl
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187	11	37.9	35	2	US-08-142-551B-5	Sequence 5, Appli
188	11	37.9	35	2	US-08-142-551B-7	Sequence 7, Appli
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258	11	37.9	35	2	US-08-142-551B-110	Sequence 110, App
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261	11	37.9	35	2	US-08-142-551B-113	Sequence 113, App
262	11	37.9	35	2	US-08-142-551B-114	Sequence 114, App
263	11	37.9	35	2	US-08-142-551B-115	Sequence 115, App
264	11	37.9	35	2	US-08-142-551B-116	Sequence 116, App
265	11	37.9	35	2	US-08-142-551B-117	Sequence 117, App
266	11	37.9	35	2	US-08-142-551B-118	Sequence 118, App
267	11	37.9	35	2	US-08-142-551B-122	Sequence 122, App
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272	10	34.5	34	3	US-09-044-536A-24	Sequence 24, Appl
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276	10	34.5	35	2	US-08-142-551B-71	Sequence 71, Appl
277	10	34.5	35	2	US-08-142-551B-101	Sequence 101, App
278	10	34.5	35	2	US-08-142-551B-102	Sequence 102, App
279	10	34.5	35	2	US-08-142-551B-103	Sequence 103, App
280	10	34.5	35	2	US-08-142-551B-120	Sequence 120, App
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282	9	31.0	28	4	US-09-228-990-62	Sequence 62, Appl
283	9	31.0	28	4	US-09-228-990-65	Sequence 65, Appl
284	9	31.0	28	4	US-09-228-990-79	Sequence 79, Appl
285	9	31.0	28	4	US-09-442-989-22	Sequence 22, Appl
286	9	31.0	28	4	US-09-442-989-25	Sequence 25, Appl
287	9	31.0	29	4	US-09-406-813-8	Sequence 8, Appli
288	9	31.0	29	4	US-09-228-990-53	Sequence 53, Appl
289	9	31.0	29	4	US-09-228-990-63	Sequence 63, Appl
290	9	31.0	30	4	US-09-228-990-52	Sequence 52, Appl
291	9	31.0	30	4	US-09-228-990-64	Sequence 64, Appl
292	9	31.0	31	3	US-08-904-760B-13	Sequence 13, Appl
293	9	31.0	31	4	US-09-228-990-3	Sequence 3, Appli
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295	9	31.0	31	4	US-09-228-990-5	Sequence 5, Appli
296	9	31.0	31	4	US-09-228-990-6	Sequence 6, Appli

297	9	31.0	31	4	US-09-228-990-7	Sequence 7, Appli
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315	9	31.0	31	4	US-09-228-990-49	Sequence 49, Appl
316	9	31.0	31	4	US-09-228-990-50	Sequence 50, Appl
317	9	31.0	31	4	US-09-228-990-51	Sequence 51, Appl
318	9	31.0	31	4	US-09-228-990-69	Sequence 69, Appl
319	9	31.0	31	4	US-09-228-990-70	Sequence 70, Appl
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322	9	31.0	31	4	US-09-228-990-82	Sequence 82, Appl
323	9	31.0	31	4	US-09-228-990-83	Sequence 83, Appl
324	9	31.0	31	4	US-09-228-990-84	Sequence 84, Appl
325	9	31.0	31	4	US-09-228-990-85	Sequence 85, Appl
326	9	31.0	31	4	US-09-536-785A-13	Sequence 13, Appl
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332	9	31.0	31	4	US-09-442-989-6	Sequence 6, Appli
333	9	31.0	31	4	US-09-442-989-7	Sequence 7, Appli
334	9	31.0	31	4	US-09-442-989-8	Sequence 8, Appli
335	9	31.0	31	4	US-09-442-989-17	Sequence 17, Appl
336	9	31.0	31	4	US-09-442-989-32	Sequence 32, Appl
337	9	31.0	34	3	US-09-044-536A-2	Sequence 2, Appli
338	9	31.0	34	3	US-09-044-536A-23	Sequence 23, Appl
339	9	31.0	34	4	US-09-228-990-46	Sequence 46, Appl
340	9	31.0	34	4	US-09-442-989-18	Sequence 18, Appl
341	9	31.0	34	4	US-09-442-989-46	Sequence 46, Appl
342	9	31.0	35	2	US-08-142-551B-72	Sequence 72, Appl
343	9	31.0	35	2	US-08-142-551B-74	Sequence 74, Appl
344	9	31.0	35	2	US-08-142-551B-75	Sequence 75, Appl
345	9	31.0	35	2	US-08-142-551B-76	Sequence 76, Appl
346	9	31.0	35	2	US-08-142-551B-77	Sequence 77, Appl
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351	9	31.0	35	2	US-08-142-551B-83	Sequence 83, Appl
352	9	31.0	35	2	US-08-142-551B-84	Sequence 84, Appl
353	9	31.0	35	2	US-08-142-551B-85	Sequence 85, Appl

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357	9	31.0	35	2	US-08-142-551B-89	Sequence 89, Appl
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359	9	31.0	35	2	US-08-142-551B-92	Sequence 92, Appl
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361	9	31.0	35	2	US-08-142-551B-95	Sequence 95, Appl
362	9	31.0	35	2	US-08-142-551B-96	Sequence 96, Appl
363	9	31.0	35	2	US-08-142-551B-97	Sequence 97, Appl
364	9	31.0	35	2	US-08-142-551B-98	Sequence 98, Appl
365	9	31.0	35	2	US-08-142-551B-99	Sequence 99, Appl
366	9	31.0	35	2	US-08-142-551B-100	Sequence 100, App
367	9	31.0	35	2	US-08-142-551B-123	Sequence 123, App
368	9	31.0	35	3	US-09-044-536A-30	Sequence 30, Appl
369	9	31.0	36	3	US-09-044-536A-31	Sequence 31, Appl
370	9	31.0	37	3	US-09-044-536A-32	Sequence 32, Appl
371	9	31.0	38	3	US-09-044-536A-33	Sequence 33, Appl
372	9	31.0	39	3	US-09-044-536A-34	Sequence 34, Appl
373	9	31.0	40	3	US-09-044-536A-35	Sequence 35, Appl
374	8	27.6	28	4	US-09-228-990-78	Sequence 78, Appl
375	8	27.6	28	4	US-09-442-989-24	Sequence 24, Appl
376	8	27.6	29	1	US-07-778-926-6	Sequence 6, Appli
377	8	27.6	30	1	US-07-778-926-10	Sequence 10, Appl
378	8	27.6	31	1	US-07-778-926-14	Sequence 14, Appl
379	8	27.6	31	4	US-09-228-990-11	Sequence 11, Appl
380	8	27.6	31	4	US-09-228-990-19	Sequence 19, Appl
381	8	27.6	31	4	US-09-228-990-28	Sequence 28, Appl
382	8	27.6	31	4	US-09-228-990-35	Sequence 35, Appl
383	8	27.6	31	4	US-09-228-990-40	Sequence 40, Appl
384	8	27.6	31	4	US-09-228-990-45	Sequence 45, Appl
385	8	27.6	31	4	US-09-228-990-66	Sequence 66, Appl
386	8	27.6	31	4	US-09-228-990-67	Sequence 67, Appl
387	8	27.6	31	4	US-09-228-990-68	Sequence 68, Appl
388	8	27.6	31	4	US-09-228-990-73	Sequence 73, Appl
389	8	27.6	31	4	US-09-228-990-76	Sequence 76, Appl
390	8	27.6	31	4	US-09-228-990-80	Sequence 80, Appl
391	8	27.6	31	4	US-09-442-989-16	Sequence 16, Appl
392	8	27.6	32	1	US-07-778-926-18	Sequence 18, Appl
393	8	27.6	33	1	US-07-778-926-7	Sequence 7, Appli
394	8	27.6	34	1	US-07-778-926-11	Sequence 11, Appl
395	8	27.6	34	1	US-07-773-098-3	Sequence 3, Appli
396	8	27.6	34	1	US-07-773-098-4	Sequence 4, Appli
397	8	27.6	34	3	US-08-903-497A-5	Sequence 5, Appli
398	8	27.6	34	4	US-09-635-076-5	Sequence 5, Appli
399	8	27.6	34	4	US-09-228-990-75	Sequence 75, Appl
400	8	27.6	34	4	US-09-442-989-19	Sequence 19, Appl
401	8	27.6	35	1	US-07-778-926-15	Sequence 15, Appl
402	8	27.6	36	1	US-07-778-926-19	Sequence 19, Appl
403	8	27.6	37	1	US-07-778-926-8	Sequence 8, Appli
404	8	27.6	38	1	US-07-778-926-12	Sequence 12, Appl
405	8	27.6	39	1	US-07-778-926-16	Sequence 16, Appl
406	8	27.6	40	1	US-07-778-926-20	Sequence 20, Appl
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408	7	24.1	31	4	US-09-406-813-9	Sequence 9, Appli
409	7	24.1	31	4	US-09-228-990-12	Sequence 12, Appl
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412	7	24.1	31	4	US-09-228-990-34	Sequence 34, Appl
413	7	24.1	31	4	US-09-228-990-41	Sequence 41, Appl
414	7	24.1	31	4	US-09-228-990-44	Sequence 44, Appl
415	7	24.1	31	4	US-09-442-989-9	Sequence 9, Appli
416	7	24.1	31	4	US-09-442-989-15	Sequence 15, Appl
417	7	24.1	32	1	US-07-778-926-3	Sequence 3, Appli
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419	7	24.1	32	1	US-08-305-799A-2	Sequence 2, Appli
420	7	24.1	34	1	US-07-915-247A-23	Sequence 23, Appl
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423	7	24.1	34	1	US-08-443-863-24	Sequence 24, Appl
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425	7	24.1	34	1	US-08-448-070-24	Sequence 24, Appl
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427	7	24.1	34	1	US-08-488-105-12	Sequence 12, Appl
428	7	24.1	34	1	US-08-488-105-17	Sequence 17, Appl
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430	7	24.1	34	1	US-08-468-275-8	Sequence 8, Appli
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433	7	24.1	34	1	US-08-449-500-35	Sequence 35, Appl
434	7	24.1	34	1	US-08-449-500-36	Sequence 36, Appl
435	7	24.1	34	1	US-08-449-500-61	Sequence 61, Appl
436	7	24.1	34	1	US-08-449-317A-23	Sequence 23, Appl
437	7	24.1	34	1	US-08-449-317A-24	Sequence 24, Appl
438	7	24.1	34	1	US-08-449-317A-35	Sequence 35, Appl
439	7	24.1	34	1	US-08-449-317A-36	Sequence 36, Appl
440	7	24.1	34	1	US-08-449-317A-61	Sequence 61, Appl
441	7	24.1	34	2	US-08-477-022-23	Sequence 23, Appl
442	7	24.1	34	2	US-08-477-022-24	Sequence 24, Appl
443	7	24.1	34	2	US-08-477-022-35	Sequence 35, Appl
444	7	24.1	34	2	US-08-477-022-36	Sequence 36, Appl
445	7	24.1	34	2	US-08-477-022-61	Sequence 61, Appl
446	7	24.1	34	2	US-08-449-447-23	Sequence 23, Appl
447	7	24.1	34	2	US-08-449-447-24	Sequence 24, Appl
448	7	24.1	34	2	US-08-449-447-35	Sequence 35, Appl
449	7	24.1	34	2	US-08-449-447-36	Sequence 36, Appl
450	7	24.1	34	2	US-08-449-447-61	Sequence 61, Appl
451	7	24.1	34	2	US-08-184-328-23	Sequence 23, Appl
452	7	24.1	34	2	US-08-184-328-24	Sequence 24, Appl
453	7	24.1	34	2	US-08-184-328-35	Sequence 35, Appl
454	7	24.1	34	2	US-08-184-328-36	Sequence 36, Appl
455	7	24.1	34	2	US-08-184-328-61	Sequence 61, Appl
456	7	24.1	34	2	US-08-521-097-23	Sequence 23, Appl
457	7	24.1	34	2	US-08-521-097-24	Sequence 24, Appl
458	7	24.1	34	2	US-08-521-097-35	Sequence 35, Appl
459	7	24.1	34	2	US-08-521-097-36	Sequence 36, Appl
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465	7	24.1	35	2	US-08-142-551B-121	Sequence 121, App
466	7	24.1	35	2	US-08-142-551B-124	Sequence 124, App
467	7	24.1	35	4	US-08-952-980B-7	Sequence 7, Appli

468	7	24.1	35	4	US-08-952-980B-8	Sequence 8, Appli
469	7	24.1	36	1	US-07-778-926-4	Sequence 4, Appli
470	6	20.7	30	4	US-09-536-785A-23	Sequence 23, Appl
471	6	20.7	31	3	US-08-904-760B-23	Sequence 23, Appl
472	6	20.7	31	4	US-09-406-813-7	Sequence 7, Appli
473	6	20.7	31	4	US-09-228-990-13	Sequence 13, Appl
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475	6	20.7	31	4	US-09-228-990-15	Sequence 15, Appl
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477	6	20.7	31	4	US-09-228-990-17	Sequence 17, Appl
478	6	20.7	31	4	US-09-228-990-30	Sequence 30, Appl
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480	6	20.7	31	4	US-09-228-990-32	Sequence 32, Appl
481	6	20.7	31	4	US-09-228-990-33	Sequence 33, Appl
482	6	20.7	31	4	US-09-228-990-42	Sequence 42, Appl
483	6	20.7	31	4	US-09-228-990-43	Sequence 43, Appl
484	6	20.7	31	4	US-09-228-990-86	Sequence 86, Appl
485	6	20.7	31	4	US-09-228-990-87	Sequence 87, Appl
486	6	20.7	31	4	US-09-228-990-88	Sequence 88, Appl
487	6	20.7	31	4	US-09-536-785A-36	Sequence 36, Appl
488	6	20.7	31	4	US-09-442-989-10	Sequence 10, Appl
489	6	20.7	31	4	US-09-442-989-11	Sequence 11, Appl
490	6	20.7	31	4	US-09-442-989-12	Sequence 12, Appl
491	6	20.7	31	4	US-09-442-989-13	Sequence 13, Appl
492	6	20.7	31	4	US-09-442-989-14	Sequence 14, Appl
493	6	20.7	32	4	US-09-536-785A-37	Sequence 37, Appl
494	6	20.7	33	4	US-09-536-785A-38	Sequence 38, Appl
495	6	20.7	34	1	US-07-765-373-2	Sequence 2, Appli
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497	6	20.7	34	1	US-08-526-987-1	Sequence 1, Appli
498	6	20.7	34	3	US-08-903-497A-6	Sequence 6, Appli
499	6	20.7	34	4	US-09-635-076-6	Sequence 6, Appli
500	6	20.7	34	4	US-09-536-785A-24	Sequence 24, Appl
501	6	20.7	35	4	US-09-536-785A-25	Sequence 25, Appl
502	6	20.7	36	4	US-09-536-785A-26	Sequence 26, Appl
503	6	20.7	37	4	US-09-536-785A-27	Sequence 27, Appl
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505	5	17.2	30	1	US-08-305-799A-9	Sequence 9, Appli
506	5	17.2	30	1	US-08-305-799A-10	Sequence 10, Appl
507	5	17.2	30	1	US-08-305-799A-11	Sequence 11, Appl
508	5	17.2	30	1	US-08-305-799A-12	Sequence 12, Appl
509	5	17.2	34	1	US-08-449-500-37	Sequence 37, Appl
510	5	17.2	34	1	US-08-449-317A-37	Sequence 37, Appl
511	5	17.2	34	2	US-08-477-022-37	Sequence 37, Appl
512	5	17.2	34	2	US-08-449-447-37	Sequence 37, Appl
513	5	17.2	34	2	US-08-184-328-37	Sequence 37, Appl
514	5	17.2	34	2	US-08-521-097-37	Sequence 37, Appl
515	5	17.2	38	1	US-08-444-005-19	Sequence 19, Appl
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518	4	13.8	28	2	US-08-185-949B-76	Sequence 76, Appl
519	4	13.8	28	2	US-08-818-253-22	Sequence 22, Appl
520	4	13.8	28	3	US-08-641-873-8	Sequence 8, Appli
521	4	13.8	28	3	US-08-818-252-22	Sequence 22, Appl
522	4	13.8	28	4	US-08-842-322-16	Sequence 16, Appl
523	4	13.8	28	4	US-09-316-919-38	Sequence 38, Appl
524	4	13.8	28	4	US-09-323-867A-153	Sequence 153, App

525	4	13.8	28	5	PCT-US92-07813-3	Sequence 3, Appli
526	4	13.8	29	1	US-08-188-582-33	Sequence 33, Appl
527	4	13.8	29	1	US-08-646-715-33	Sequence 33, Appl
528	4	13.8	29	4	US-09-227-357-386	Sequence 386, App
529	4	13.8	29	4	US-09-695-458-8	Sequence 8, Appli
530	4	13.8	29	4	US-09-205-258-1006	Sequence 1006, Ap
531	4	13.8	30	1	US-08-305-799A-3	Sequence 3, Appli
532	4	13.8	30	1	US-08-305-799A-4	Sequence 4, Appli
533	4	13.8	30	4	US-09-205-258-821	Sequence 821, App
534	4	13.8	31	1	US-07-829-462-3	Sequence 3, Appli
535	4	13.8	31	1	US-08-340-812-3	Sequence 3, Appli
536	4	13.8	31	1	US-08-248-021A-5	Sequence 5, Appli
537	4	13.8	31	1	US-08-323-531-44	Sequence 44, Appl
538	4	13.8	31	1	US-08-323-531-50	Sequence 50, Appl
539	4	13.8	31	1	US-08-323-531-62	Sequence 62, Appl
540	4	13.8	31	1	US-08-198-094-44	Sequence 44, Appl
541	4	13.8	31	1	US-08-198-094-50	Sequence 50, Appl
542	4	13.8	31	1	US-08-198-094-62	Sequence 62, Appl
543	4	13.8	31	1	US-08-459-064B-3	Sequence 3, Appli
544	4	13.8	31	2	US-08-460-421A-3	Sequence 3, Appli
545	4	13.8	31	2	US-08-663-566A-32	Sequence 32, Appl
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547	4	13.8	31	2	US-08-288-065A-32	Sequence 32, Appl
548	4	13.8	31	2	US-08-362-240A-32	Sequence 32, Appl
549	4	13.8	31	3	US-08-107-794A-44	Sequence 44, Appl
550	4	13.8	31	3	US-08-107-794A-50	Sequence 50, Appl
551	4	13.8	31	3	US-08-107-794A-62	Sequence 62, Appl
552	4	13.8	31	4	US-09-205-258-1001	Sequence 1001, Ap
553	4	13.8	31	5	PCT-US93-00909-3	Sequence 3, Appli
554	4	13.8	31	5	PCT-US93-07424-44	Sequence 44, Appl
555	4	13.8	31	5	PCT-US93-07424-50	Sequence 50, Appl
556	4	13.8	31	5	PCT-US93-07424-62	Sequence 62, Appl
557	4	13.8	31	5	PCT-US95-02087-44	Sequence 44, Appl
558	4	13.8	31	5	PCT-US95-02087-50	Sequence 50, Appl
559	4	13.8	31	5	PCT-US95-02087-62	Sequence 62, Appl
560	4	13.8	31	5	PCT-US95-10245-32	Sequence 32, Appl
561	4	13.8	32	1	US-08-190-802A-110	Sequence 110, App
562	4	13.8	32	1	US-08-190-802A-114	Sequence 114, App
563	4	13.8	32	1	US-08-190-802A-183	Sequence 183, App
564	4	13.8	32	1	US-08-190-802A-216	Sequence 216, App
565	4	13.8	32	3	US-08-477-346-110	Sequence 110, App
566	4	13.8	32	3	US-08-477-346-114	Sequence 114, App
567	4	13.8	32	3	US-08-477-346-183	Sequence 183, App
568	4	13.8	32	3	US-08-477-346-216	Sequence 216, App
569	4	13.8	32	4	US-08-473-089-110	Sequence 110, App
570	4	13.8	32	4	US-08-473-089-114	Sequence 114, App
571	4	13.8	32	4	US-08-473-089-183	Sequence 183, App
572	4	13.8	32	4	US-08-473-089-216	Sequence 216, App
573	4	13.8	32	4	US-09-149-476-442	Sequence 442, App
574	4	13.8	32	4	US-08-487-072A-110	Sequence 110, App
575	4	13.8	32	4	US-08-487-072A-114	Sequence 114, App
576	4	13.8	32	4	US-08-487-072A-183	Sequence 183, App
577	4	13.8	32	4	US-08-487-072A-216	Sequence 216, App
578	4	13.8	33	1	US-08-781-020-10	Sequence 10, Appl
579	4	13.8	33	3	US-09-038-935-10	Sequence 10, Appl
580	4	13.8	33	4	US-09-149-476-660	Sequence 660, App
581	4	13.8	33	4	US-09-122-144-4	Sequence 4, Appli

582	4	13.8	33	4	US-09-205-258-368	Sequence 368, App
583	4	13.8	34	1	US-08-007-775-1	Sequence 1, Appli
584	4	13.8	34	1	US-07-956-700B-7	Sequence 7, Appli
585	4	13.8	34	1	US-08-476-537-7	Sequence 7, Appli
586	4	13.8	34	1	US-08-485-607-7	Sequence 7, Appli
587	4	13.8	34	2	US-08-475-879-7	Sequence 7, Appli
588	4	13.8	34	4	US-09-433-043B-7	Sequence 7, Appli
589	4	13.8	35	1	US-08-463-660-6	Sequence 6, Appli
590	4	13.8	35	1	US-08-678-280-6	Sequence 6, Appli
591	4	13.8	35	4	US-09-690-454-138	Sequence 138, App
592	4	13.8	36	1	US-08-477-727A-104	Sequence 104, App
593	4	13.8	36	1	US-08-471-675A-26	Sequence 26, Appl
594	4	13.8	36	2	US-08-892-549-30	Sequence 30, Appl
595	4	13.8	36	3	US-08-302-069A-25	Sequence 25, Appl
596	4	13.8	37	1	US-08-231-730A-45	Sequence 45, Appl
597	4	13.8	37	1	US-08-477-727A-102	Sequence 102, App
598	4	13.8	37	1	US-08-477-727A-103	Sequence 103, App
599	4	13.8	37	1	US-08-477-727A-105	Sequence 105, App
600	4	13.8	37	1	US-08-477-727A-106	Sequence 106, App
601	4	13.8	37	1	US-08-477-727A-107	Sequence 107, App
602	4	13.8	37	1	US-08-471-675A-24	Sequence 24, Appl
603	4	13.8	37	1	US-08-471-675A-25	Sequence 25, Appl
604	4	13.8	37	1	US-08-471-675A-27	Sequence 27, Appl
605	4	13.8	37	1	US-08-471-675A-28	Sequence 28, Appl
606	4	13.8	37	1	US-08-471-675A-29	Sequence 29, Appl
607	4	13.8	37	2	US-08-259-762-12	Sequence 12, Appl
608	4	13.8	37	2	US-08-259-762-13	Sequence 13, Appl
609	4	13.8	37	2	US-08-283-917-12	Sequence 12, Appl
610	4	13.8	37	2	US-08-961-716-12	Sequence 12, Appl
611	4	13.8	37	2	US-08-505-486-50	Sequence 50, Appl
612	4	13.8	37	2	US-08-892-549-6	Sequence 6, Appli
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614	4	13.8	37	2	US-08-892-549-29	Sequence 29, Appl
615	4	13.8	37	2	US-08-892-549-31	Sequence 31, Appl
616	4	13.8	37	2	US-08-892-549-32	Sequence 32, Appl
617	4	13.8	37	2	US-08-892-549-33	Sequence 33, Appl
618	4	13.8	37	3	US-08-689-489C-45	Sequence 45, Appl
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620	4	13.8	37	3	US-09-340-154-50	Sequence 50, Appl
621	4	13.8	37	3	US-08-302-069A-23	Sequence 23, Appl
622	4	13.8	37	3	US-08-302-069A-24	Sequence 24, Appl
623	4	13.8	37	3	US-08-302-069A-26	Sequence 26, Appl
624	4	13.8	37	3	US-08-302-069A-27	Sequence 27, Appl
625	4	13.8	37	3	US-08-302-069A-28	Sequence 28, Appl
626	4	13.8	37	3	US-09-232-802A-45	Sequence 45, Appl
627	4	13.8	37	4	US-09-482-611B-50	Sequence 50, Appl
628	4	13.8	37	5	PCT-US95-04718-45	Sequence 45, Appl
629	4	13.8	37	5	PCT-US95-09338-50	Sequence 50, Appl
630	4	13.8	37	5	PCT-US95-09339-50	Sequence 50, Appl
631	4	13.8	38	1	US-07-781-254A-18	Sequence 18, Appl
632	4	13.8	38	2	US-08-378-548-12	Sequence 12, Appl
633	4	13.8	39	4	US-09-227-357-384	Sequence 384, App
634	4	13.8	39	4	US-09-323-867A-25	Sequence 25, Appl
635	3	10.3	28	1	US-07-620-410-2	Sequence 2, Appli
636	3	10.3	28	1	US-07-690-300B-1	Sequence 1, Appli
637	3	10.3	28	1	US-07-690-300B-12	Sequence 12, Appl
638	3	10.3	28	1	US-07-690-300B-23	Sequence 23, Appl

639	3	10.3	28	1	US-07-690-300B-24	Sequence 24, Appl
640	3	10.3	28	1	US-07-690-300B-25	Sequence 25, Appl
641	3	10.3	28	1	US-07-690-300B-26	Sequence 26, Appl
642	3	10.3	28	1	US-07-690-300B-27	Sequence 27, Appl
643	3	10.3	28	1	US-07-690-300B-28	Sequence 28, Appl
644	3	10.3	28	1	US-07-690-300B-29	Sequence 29, Appl
645	3	10.3	28	1	US-07-690-300B-30	Sequence 30, Appl
646	3	10.3	28	1	US-07-690-300B-31	Sequence 31, Appl
647	3	10.3	28	1	US-07-690-300B-32	Sequence 32, Appl
648	3	10.3	28	1	US-07-690-300B-33	Sequence 33, Appl
649	3	10.3	28	1	US-07-690-300B-34	Sequence 34, Appl
650	3	10.3	28	1	US-07-690-300B-35	Sequence 35, Appl
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677	3	10.3	28	1	US-07-690-300B-79	Sequence 79, Appl
678	3	10.3	28	1	US-07-690-300B-82	Sequence 82, Appl
679	3	10.3	28	1	US-07-690-300B-88	Sequence 88, Appl
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831	3	10.3	28	2	US-08-621-803-143	Sequence 143, App
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841	3	10.3	28	2	US-08-621-259A-113	Sequence 113, App
842	3	10.3	28	2	US-08-621-259A-114	Sequence 114, App
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859	3	10.3	28	2	US-08-413-708B-8	Sequence 8, Appli
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862	3	10.3	28	2	US-08-818-253-37	Sequence 37, Appl
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864	3	10.3	28	2	US-08-897-624-2	Sequence 2, Appli
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871	3	10.3	28	3	US-08-788-231A-18	Sequence 18, Appl
872	3	10.3	28	3	US-08-484-223B-84	Sequence 84, Appl
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915	3	10.3	28	3	US-08-657-162-195	Sequence 195, App
916	3	10.3	28	3	US-08-657-162-196	Sequence 196, App
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931	3	10.3	28	3	US-08-985-499-39	Sequence 39, Appl
932	3	10.3	28	3	US-08-818-252-37	Sequence 37, Appl
933	3	10.3	28	3	US-08-363-558-1	Sequence 1, Appli
934	3	10.3	28	3	US-09-066-046-19	Sequence 19, Appl
935	3	10.3	28	3	US-09-253-396A-223	Sequence 223, App
936	3	10.3	28	3	US-09-107-991-12	Sequence 12, Appl
937	3	10.3	28	3	US-09-093-539-12	Sequence 12, Appl
938	3	10.3	28	3	US-09-093-539-56	Sequence 56, Appl
939	3	10.3	28	3	US-08-485-264A-84	Sequence 84, Appl
940	3	10.3	28	3	US-08-485-264A-136	Sequence 136, App
941	3	10.3	28	3	US-09-303-323-38	Sequence 38, Appl
942	3	10.3	28	3	US-09-041-886-36	Sequence 36, Appl
943	3	10.3	28	3	US-09-041-886-37	Sequence 37, Appl
944	3	10.3	28	3	US-09-041-886-38	Sequence 38, Appl
945	3	10.3	28	3	US-09-041-886-39	Sequence 39, Appl
946	3	10.3	28	3	US-09-041-886-40	Sequence 40, Appl
947	3	10.3	28	3	US-09-041-886-42	Sequence 42, Appl
948	3	10.3	28	3	US-09-041-886-47	Sequence 47, Appl
949	3	10.3	28	3	US-09-041-886-50	Sequence 50, Appl
950	3	10.3	28	3	US-09-041-886-53	Sequence 53, Appl
951	3	10.3	28	3	US-09-041-886-54	Sequence 54, Appl
952	3	10.3	28	3	US-09-041-886-56	Sequence 56, Appl
953	3	10.3	28	3	US-09-127-680-2	Sequence 2, Appli
954	3	10.3	28	3	US-07-966-049A-9	Sequence 9, Appli
955	3	10.3	28	3	US-08-995-369-1	Sequence 1, Appli
956	3	10.3	28	3	US-09-171-654-1	Sequence 1, Appli
957	3	10.3	28	3	US-08-605-430-43	Sequence 43, Appl
958	3	10.3	28	3	US-08-894-327-22	Sequence 22, Appl
959	3	10.3	28	3	US-09-082-279B-54	Sequence 54, Appl
960	3	10.3	28	3	US-09-082-279B-62	Sequence 62, Appl
961	3	10.3	28	3	US-09-082-279B-1279	Sequence 1279, Ap
962	3	10.3	28	3	US-09-082-279B-1280	Sequence 1280, Ap
963	3	10.3	28	3	US-09-082-279B-1314	Sequence 1314, Ap
964	3	10.3	28	3	US-09-082-279B-1315	Sequence 1315, Ap
965	3	10.3	28	3	US-08-477-346-84	Sequence 84, Appl
966	3	10.3	28	3	US-08-942-046-34	Sequence 34, Appl
967	3	10.3	28	3	US-08-894-997-43	Sequence 43, Appl
968	3	10.3	28	3	US-09-217-352-30	Sequence 30, Appl
969	3	10.3	28	3	US-09-217-352-139	Sequence 139, App
970	3	10.3	28	3	US-09-217-352-140	Sequence 140, App
971	3	10.3	28	3	US-09-217-352-142	Sequence 142, App
972	3	10.3	28	3	US-09-217-352-143	Sequence 143, App
973	3	10.3	28	3	US-09-019-095A-34	Sequence 34, Appl
974	3	10.3	28	4	US-09-260-846-16	Sequence 16, Appl
975	3	10.3	28	4	US-08-474-349A-84	Sequence 84, Appl
976	3	10.3	28	4	US-08-474-349A-136	Sequence 136, App
977	3	10.3	28	4	US-09-099-041A-19	Sequence 19, Appl
978	3	10.3	28	4	US-09-099-041A-23	Sequence 23, Appl
979	3	10.3	28	4	US-09-187-789-23	Sequence 23, Appl
980	3	10.3	28	4	US-08-473-089-84	Sequence 84, Appl

981	3	10.3	28	4	US-09-227-357-481	Sequence 481, App
982	3	10.3	28	4	US-09-315-304B-54	Sequence 54, Appl
983	3	10.3	28	4	US-09-315-304B-62	Sequence 62, Appl
984	3	10.3	28	4	US-09-315-304B-1279	Sequence 1279, Ap
985	3	10.3	28	4	US-09-315-304B-1280	Sequence 1280, Ap
986	3	10.3	28	4	US-09-315-304B-1314	Sequence 1314, Ap
987	3	10.3	28	4	US-09-315-304B-1315	Sequence 1315, Ap
988	3	10.3	28	4	US-09-432-879-8	Sequence 8, Appli
989	3	10.3	28	4	US-08-979-608A-26	Sequence 26, Appl
990	3	10.3	28	4	US-09-245-281-19	Sequence 19, Appl
991	3	10.3	28	4	US-09-245-281-23	Sequence 23, Appl
992	3	10.3	28	4	US-08-842-322-31	Sequence 31, Appl
993	3	10.3	28	4	US-09-280-909A-19	Sequence 19, Appl
994	3	10.3	28	4	US-09-333-842-1	Sequence 1, Appli
995	3	10.3	28	4	US-09-685-027-22	Sequence 22, Appl
996	3	10.3	28	4	US-08-487-072A-84	Sequence 84, Appl
997	3	10.3	28	4	US-09-446-352B-1	Sequence 1, Appli
998	3	10.3	28	4	US-09-139-600-18	Sequence 18, Appl
999	3	10.3	28	4	US-09-288-143-131	Sequence 131, App
1000	3	10.3	28	4	US-08-255-208A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-262-495C-5

; Sequence 5, Application US/08262495C

; Patent No. 5556940

; GENERAL INFORMATION:

; APPLICANT: WILICK, Gordon E.

; APPLICANT: WHITFIELD, James F.

; APPLICANT: SUREWICZ, Witold

; APPLICANT: SUNG, Wing L.

; APPLICANT: NEUGENBAUER, Witold

; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kirby, Eades, Gale, Baker

; STREET: 112 Kent Street, Suite 770,

; CITY: Ottawa

; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/262,495C

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-262-495C-5

Query Match 100.0%; Score 29; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 2

US-08-262-495C-3

; Sequence 3, Application US/08262495C
; Patent No. 5556940

; GENERAL INFORMATION:

; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa
; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263

; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-262-495C-3

Query Match 100.0%; Score 29; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 3

US-08-691-647C-1

; Sequence 1, Application US/08691647C
; Patent No. 5955425
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 New York Avenue, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,647C
; FILING DATE: August 2, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4005

```

;      TELEFAX:  (703) 816-4100
;      TELEX:    N/A
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:   31 amino acids
;      TYPE:     amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE:  protein
US-08-691-647C-1

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Query Match 100.0%; Score 29; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRRKKLO 29

RESULT 4

US-08-691-647C-6

; Sequence 6, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue, 8th Floor

CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: ASCII Text
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; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/691,647C

FILING DATE: August 2, 1996

CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: cyclic
; MOLECULE TYPE: protein
US-08-691-647C-6

Query Match 100.0%; Score 29; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 5

US-08-904-760B-1

; Sequence 1, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-904-760B-1

Query Match 100.0%; Score 29; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 6

US-08-904-760B-6

; Sequence 6, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 6:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 31 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: circular
; MOLECULE TYPE: protein
; FEATURE:
;   OTHER INFORMATION: cyclo Lys27-Asp30, and this sequence
;   OTHER INFORMATION: has an amino group c-terminus (NH2).
US-08-904-760B-6

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Query Match          100.0%; Score 29; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

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RESULT 7

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US-08-904-760B-14
; Sequence 14, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
;   APPLICANT: Jean-Rene, Barbier
;   APPLICANT: Neugebauer, Witold
;   APPLICANT: Ross, Virginia
;   APPLICANT: Whitfield, James
;   APPLICANT: Willick, Gordon E.
;   TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
;   TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: NIXON & VANDERHYE P.C.
;   STREET: 1100 No. 6110892th Glebe Rd. 8th floor
;   CITY: Arlington
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22201-4741
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/904,760B
;   FILING DATE: 01-AUG-1997
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/691,647
;   FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Crawford, Arthur R.
;   REGISTRATION NUMBER: 25,327
;   REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:

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; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 1339-6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; OTHER INFORMATION: This sequence has an amino group
 ; OTHER INFORMATION: c-terminus (NH2).
 US-08-904-760B-32

Query Match 100.0%; Score 29; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 9

US-09-406-813-2
 ; Sequence 2, Application US/09406813
 ; Patent No. 6316410
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbier, Jean-Rene
 ; APPLICANT: Morley, Paul
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 10688-1B
 ; CURRENT APPLICATION NUMBER: US/09/406,813
 ; CURRENT FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: 08/904,760
 ; PRIOR FILING DATE: 1997-08-01
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: This sequence has an amino group c-terminus (NH2).
 US-09-406-813-2

Query Match 100.0%; Score 29; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Db |||||
1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 10

US-09-536-785A-1

; Sequence 1, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-536-785A-1

Query Match 100.0%; Score 29; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 11

US-09-536-785A-6

; Sequence 6, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF

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; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)..(30)
; OTHER INFORMATION: Cyclo Lys27-Asp30
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-6
```

```
Query Match          100.0%; Score 29; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 12

```
US-09-536-785A-14
; Sequence 14, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
```


Query Match 100.0%; Score 29; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Dd

1 SVSEIQLMHNLGKHLNSMERVEWLRKKLO 29

RESULT 14

```

US-09-447-800-9
; Sequence 9, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;   APPLICANT: BRINGHURST, F. RICHARD
;   APPLICANT: TAKASU, HISASHI
;   APPLICANT: GARDELLA, THOMAS J.
;   TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;   TITLE OF INVENTION: ANALOGS
;   FILE REFERENCE: 0609.4630001
;   CURRENT APPLICATION NUMBER: US/09/447,800
;   CURRENT FILING DATE: 1999-11-23
;   EARLIER APPLICATION NUMBER: 60/110,152
;   EARLIER FILING DATE: 1998-11-25
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ser
US-09-447-800-9

```

Query Match 100.0%; Score 29; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 15

US-07-765-373-1
; Sequence 1, Application US/07765373
; Patent No. 5393869
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: KAWASE, Masahiro
; APPLICANT: YAMAZAKI, Iwao
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/765,373
; FILING DATE: 19910925
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 41289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 20091 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-07-765-373-1

```

```

Query Match          100.0%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 16

US-08-033-099-1

```

; Sequence 1, Application US/08033099
; Patent No. 5434246

```

GENERAL INFORMATION:

```

; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston

```

; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/033,099
 ; FILING DATE: 19930316
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILLIAMS, Gregory D
 ; REGISTRATION NUMBER: 30901
 ; REFERENCE/DOCKET NUMBER: 42528
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (613)523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: N-terminal
 US-08-033-099-1

Query Match 100.0%; Score 29; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 17

US-08-262-495C-1

; Sequence 1, Application US/08262495C
 ; Patent No. 5556940
 ; GENERAL INFORMATION:
 ; APPLICANT: WILICK, Gordon E.
 ; APPLICANT: WHITFIELD, James F.
 ; APPLICANT: SUREWICZ, Witold
 ; APPLICANT: SUNG, Wing L.
 ; APPLICANT: NEUGENBAUER, Witold
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
 ; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kirby, Eades, Gale, Baker
 ; STREET: 112 Kent Street, Suite 770,
 ; CITY: Ottawa
 ; COUNTRY: Canada
 ; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-495C-1

```

```

Query Match          100.0%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 18

US-07-915-247A-1

```

; Sequence 1, Application US/07915247A
; Patent No. 5589452
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,247A
; FILING DATE: 19920714
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-07-915-247A-1

```

```

Query Match          100.0%;  Score 29;  DB 1;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.2e-20;
Matches 29;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 19

US-08-443-863-1

```

; Sequence 1, Application US/08443863
; Patent No. 5693616
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:

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```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,863
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-443-863-1

```

```

Query Match          100.0%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

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RESULT 20

US-08-448-070-1

```

; Sequence 1, Application US/08448070
; Patent No. 5695955
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,070
;      FILING DATE:  14-JUL-1992
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Schmonsees, William
;      REGISTRATION NUMBER:  31,796
;      REFERENCE/DOCKET NUMBER:  27610
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-6593
;      TELEFAX:  415-496-3529
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      HYPOTHETICAL:  NO
;      FRAGMENT TYPE:  N-terminal
US-08-448-070-1

```

```

Query Match          100.0%;  Score 29;  DB 1;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.2e-20;
Matches  29;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

QY      1  SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1  SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

```

RESULT 21
US-08-488-105-7
; Sequence 7, Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT:  Chorev, Michael
; APPLICANT:  Rosenblatt, Michael
; TITLE OF INVENTION:  CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES:  22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Fish & Richardson P.C.
; STREET:  225 Franklin Street
; CITY:  Boston
; STATE:  MA
; COUNTRY:  USA
; ZIP:  02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/488,105
; FILING DATE:  07-JUN-1995

```

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/112001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: The side chains of Lys at
; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an
amide bond,
; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,
CONH2), rather
; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
US-08-488-105-7

```

```

Query Match          100.0%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 22

US-08-468-275-6

```

; Sequence 6, Application US/08468275
; Patent No. 5747453

```

GENERAL INFORMATION:

```

; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/468,275
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MILLER, D. BYRON
 ; REGISTRATION NUMBER: 30,661
 ; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 496-8150
 ; TELEFAX: (415) 496-8048
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-468-275-6

Query Match 100.0%; Score 29; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 23

US-08-449-500-1

; Sequence 1, Application US/08449500
 ; Patent No. 5798225

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.
 ; APPLICANT: Nestor Jr., John J.
 ; APPLICANT: Ho, Teresa H.
 ; APPLICANT: Vickery, Brian H.
 ; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
 ; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
 ; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
 ; STREET: 3401 Hillview Ave.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,500
 ; FILING DATE: 18-JAN-1994

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Schmonsees, William
;   REGISTRATION NUMBER: 31,796
;   REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-6593
;   TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-500-1

```

```

Query Match          100.0%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 24

US-08-449-317A-1

```

; Sequence 1, Application US/08449317A
; Patent No. 5807823

```

GENERAL INFORMATION:

```

; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
;   STREET: 3401 Hillview Ave.
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94303

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/449,317A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

```

ATTORNEY/AGENT INFORMATION:

```

; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 100.0%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 25

US-08-142-551B-2

; Sequence 2, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.
 ; REGISTRATION NUMBER: 30,113
 ; REFERENCE/DOCKET NUMBER: 000324-010
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 854-7400
 ; TELEFAX: (415) 854-8275
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..34
 ; OTHER INFORMATION: /note= "The sequence of the 34
 ; OTHER INFORMATION: amino acid truncated human PTH peptide,
 ; OTHER INFORMATION: designated: Human PTH."
 US-08-142-551B-2

Query Match 100.0%; Score 29; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 26

US-08-477-022-1

; Sequence 1, Application US/08477022
 ; Patent No. 5821225
 ; GENERAL INFORMATION:
 ; APPLICANT: Vickery, Brian H.
 ; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
 ; TITLE OF INVENTION: INDUCED OSTEOPENIA
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
 ; STREET: 3401 Hillview Ave.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,022
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schmonsees, William
 ; REGISTRATION NUMBER: 31,796

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-447-1

Query Match 100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 28

US-08-835-231-13

; Sequence 13, Application US/08835231
; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991

```

; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-13

```

```

Query Match          100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 29

US-08-184-328-1

```

; Sequence 1, Application US/08184328
; Patent No. 5874086

```

GENERAL INFORMATION:

```

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.

```

```

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

```

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

```

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,328
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-184-328-1
```

```
Query Match          100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 30

```
US-08-411-726-2
; Sequence 2, Application US/08411726
; Patent No. 5880093
; GENERAL INFORMATION:
; APPLICANT: BAGNOLI, Franco
; TITLE OF INVENTION: Use of Parathormone, Its Biologically
; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The
Preparation of
; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment
of Pregnanc
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1 Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,726
```

```

; FILING DATE: 05-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/02755
; FILING DATE: 08-OCT-1993
; APPLICATION NUMBER: MI-92A002331
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PALMESE, Maria Luisa
; REGISTRATION NUMBER: 34,402
; REFERENCE/DOCKET NUMBER: 2111/1300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-425-7200
; TELEFAX: 212-425-5288
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-2

```

```

Query Match          100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 31

US-08-691-647C-5

; Sequence 5, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue, 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,647C
; FILING DATE: August 2, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4005
; TELEFAX: (703) 816-4100
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-5

```

```

Query Match          100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 32

```

US-08-521-097-1
; Sequence 1, Application US/08521097
; Patent No. 5977070
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/521,097
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,328
; FILING DATE: 18-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-521-097-1

Query Match 100.0%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 33

US-09-044-536A-1

; Sequence 1, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A

```

; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-1

```

```

Query Match          100.0%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 34

US-08-904-760B-22

; Sequence 22, Application US/08904760B
; Patent No. 6110892

; GENERAL INFORMATION:

```

; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-904-760B-22

```

```

Query Match          100.0%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 35

```

US-08-903-497A-1
; Sequence 1, Application US/08903497A
; Patent No. 6147186
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: J ppner, Harald
; TITLE OF INVENTION: No. 6147186el Parathyroid Hormone-Related
; TITLE OF INVENTION: Peptide Analogs
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/903,497A
; FILING DATE: 30-JUL-1997

```



```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,471
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
; OTHER INFORMATION: AMIDE
US-08-903-497A-1

```

```

Query Match          100.0%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 36

```

US-09-108-661-13
; Sequence 13, Application US/09108661
; Patent No. 6287806
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-13

```

```

Query Match          100.0%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 37

US-09-007-466-6

```

; Sequence 6, Application US/09007466
; Patent No. 6313092
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD

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; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94303-0802
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/007,466
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/468,275
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MILLER, D. BYRON
 ; REGISTRATION NUMBER: 30,661
 ; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 496-8150
 ; TELEFAX: (415) 496-8048
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-007-466-6

Query Match 100.0%; Score 29; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
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 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 38

US-09-406-813-1
 ; Sequence 1, Application US/09406813
 ; Patent No. 6316410
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbier, Jean-Rene
 ; APPLICANT: Morley, Paul
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 10688-1B
 ; CURRENT APPLICATION NUMBER: US/09/406,813
 ; CURRENT FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: 08/904,760
 ; PRIOR FILING DATE: 1997-08-01

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;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-406-813-1
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Query Match 100.0%; Score 29; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 39

US-08-952-980B-6

: Sequence 6, Application US/08952980B

; Patent No. 6333189

; GENERAL INFORMATION:

APPLICANT: HOLLADAY, LESLIE A.

APPLICANT: OLDENBURG, KEVIN R.

TITLE OF INVENTION: METHOD FOR INCREASING THE

TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

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NUMBER OF SEQUENCES: 12

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CORRESPONDENCE ADDRESS:

ADDRESSEE: ALZA CORPORATION

STREET: 950 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94303-0802

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

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; OPERATING SYSTEM:  PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/952,980B

FILING DATE: 20-NOV-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: MILLER, D. BYRON

REGISTRATION NUMBER: 30,661

REFERENCE/DOCKET NUMBER: 2349 CIP 1

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 496-8150

TELEFAX: (650) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

; TYPE: amino acid

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; STRANDEDNESS: single
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;      TOPOLOGY:  linear

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; MOLECULE TYPE: protein

; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
;
OTHER INFORMATION: AMIDE
US-09-635-076-1

Query Match 100.0%; Score 29; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Search completed: January 14, 2004, 10:43:36
Job time : 10.8474 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 8.58255 Seconds
 (without alignments)
 324.949 Million cell updates/sec

Title: US-09-843-221A-167
 Perfect score: 29
 Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5	17.2	34	2	B97032	transcription regu
3	4	13.8	28	2	T09594	gene LFY protein -
4	4	13.8	29	1	A55527	pyrroloquinoline q
5	4	13.8	29	2	I78537	copper transportin
6	4	13.8	29	2	S78412	ribosomal protein
7	4	13.8	30	2	S63531	hypothetical prote
8	4	13.8	31	2	S44471	glucagon G1 - Nort
9	4	13.8	31	2	S44472	glucagon G2 - Nort
10	4	13.8	31	2	D70236	hypothetical prote
11	4	13.8	32	2	F23454	ovalbumin phosphos
12	4	13.8	32	2	D31461	T-cell receptor de
13	4	13.8	33	2	E81714	hypothetical prote

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19	4	13.8	36	2	F95057	hypothetical prote
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21	4	13.8	36	2	S46227	hypothetical prote
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23	4	13.8	37	2	T12635	homeotic protein H
24	4	13.8	39	1	CKFHCS	sarcotoxin IC - fl
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27	3	10.3	28	2	C32416	phospholipase A2 (
28	3	10.3	28	2	B60071	vasoactive intesti
29	3	10.3	28	2	A60304	vasoactive intesti
30	3	10.3	28	2	S58386	T-cell receptor be
31	3	10.3	28	2	PN0047	signal transductio
32	3	10.3	28	2	S70894	hypothetical prote
33	3	10.3	28	2	S22469	hypothetical prote
34	3	10.3	28	2	S26254	rel protein - chic
35	3	10.3	28	2	I59477	antigen, T-cell re
36	3	10.3	28	2	F46522	T-cell receptor et
37	3	10.3	29	1	GCCB	glucagon - Chinci
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50	3	10.3	29	2	A27688	mammary-derived gr
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54	3	10.3	29	2	A59479	NADP phosphatase I
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57	3	10.3	30	2	A28562	glutathione transf
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61	3	10.3	30	2	S21815	H+-exporting ATPas
62	3	10.3	30	2	A44912	cysteine proteinas
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64	3	10.3	30	2	PD0013	cAMP response elem
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77	3	10.3	30	2	E82294	hypothetical prote
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80	3	10.3	30	2	S73316	photosystem I chai
81	3	10.3	30	2	A32946	trypsin-like serin
82	3	10.3	30	2	PL0189	Ig light chain - s
83	3	10.3	30	2	S65519	carcinoembryonic a
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85	3	10.3	30	2	D81532	hypothetical prote
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93	3	10.3	31	1	A49078	leiurotoxin I-like
94	3	10.3	31	1	S34504	photosystem I prot
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104	3	10.3	31	2	S38881	inner membrane pro
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120	3	10.3	31	2	A36221	cecropin P1 - pig
121	3	10.3	31	2	S27112	sarcolipin - rabbi
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139	3	10.3	32	2	S36809	GTP-binding regula
140	3	10.3	32	2	A29743	translation initia
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142	3	10.3	32	2	A44900	fimbrin, SEF 21 -
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167	3	10.3	33	2	S43312	2',3'-cyclic-nucle
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169	3	10.3	33	2	I52219	c-ras-Ki-2 protein
170	3	10.3	33	2	I53221	K-ras protein - hu
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176	3	10.3	33	2	A03150	retinoic acid-bind
177	3	10.3	33	2	C46027	neurotransmitter t
178	3	10.3	33	2	PQ0150	dnaK-type molecula
179	3	10.3	33	2	B44906	L1 protein - human
180	3	10.3	33	2	PQ0418	matrix protein M1
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193	3	10.3	34	2	A40298	dermaseptin - Sauv
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212	3	10.3	34	2	A60110	repetitive protein
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226	3	10.3	35	2	S74556	photosystem II psb
227	3	10.3	35	2	S18224	filamentous hemagg
228	3	10.3	35	2	S18226	opacity protein op
229	3	10.3	35	2	T07870	major latex protei
230	3	10.3	35	2	B33770	hypothetical prote
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238	3	10.3	35	2	H81948	hypothetical prote
239	3	10.3	35	2	A82151	hypothetical prote
240	3	10.3	35	2	F82051	hypothetical prote
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242	3	10.3	35	2	F69827	hypothetical prote
243	3	10.3	35	2	C69977	hypothetical prote
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246	3	10.3	35	2	S49309	oncofetal protein
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251	3	10.3	36	2	S72299	ribosomal protein
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253	3	10.3	36	2	I46593	myosin - pig (frag
254	3	10.3	36	2	B31872	retinoic acid-bind
255	3	10.3	36	2	S35572	zona pellucida pro
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257	3	10.3	36	2	A38659	methanol dehydroge
258	3	10.3	36	2	C95218	conserved domain p
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275	3	10.3	36	2	T22263	hypothetical prote
276	3	10.3	36	2	A57443	guanylate cyclase
277	3	10.3	36	2	D83682	hypothetical prote
278	3	10.3	36	2	A83870	hypothetical prote
279	3	10.3	36	2	F84074	hypothetical prote
280	3	10.3	36	2	A56634	neuropeptide F - A
281	3	10.3	36	2	S77071	probable plastoqui
282	3	10.3	36	2	AF1015	hypothetical prote
283	3	10.3	36	2	AI1841	hypothetical prote
284	3	10.3	37	1	S32792	iberiotoxin - east
285	3	10.3	37	1	HSWT93	histone H2A.3 - wh
286	3	10.3	37	2	S48656	fusicoccin recepto
287	3	10.3	37	2	S03570	trypsin (EC 3.4.21
288	3	10.3	37	2	S39367	proteinase omega -
289	3	10.3	37	2	S06217	transforming prote
290	3	10.3	37	2	S05037	insulinoma amyloid
291	3	10.3	37	2	A30607	Ig kappa chain V-I
292	3	10.3	37	2	PC1121	antifungal 25K pro
293	3	10.3	37	2	G01887	MEK kinase - human
294	3	10.3	37	2	S07517	gene 6.3 protein -
295	3	10.3	37	2	G70223	hypothetical prote
296	3	10.3	37	2	E70241	hypothetical prote
297	3	10.3	37	2	D83199	hypothetical prote
298	3	10.3	37	2	H82304	hypothetical prote

299	3	10.3	37	2	S21132	photosystem II cyt
300	3	10.3	37	2	F59103	hypothetical prote
301	3	10.3	37	2	T36662	small hypothetical
302	3	10.3	37	2	T11815	hypothetical prote
303	3	10.3	37	2	A57127	diuretic hormone 1
304	3	10.3	37	2	C32112	R15 gamma peptide
305	3	10.3	37	2	B48845	sterol regulatory
306	3	10.3	37	2	S68261	hypothetical prote
307	3	10.3	37	2	S49982	Tcell receptor alp
308	3	10.3	37	2	PN0550	metabotropic gluta
309	3	10.3	37	2	S70931	histone-like prote
310	3	10.3	37	2	F81403	hypothetical prote
311	3	10.3	38	1	R5EC36	ribosomal protein
312	3	10.3	38	2	C34047	stylar glycoprotei
313	3	10.3	38	2	T11763	acetyl-CoA carboxy
314	3	10.3	38	2	S39034	lipid transfer pro
315	3	10.3	38	2	A42974	natriuretic peptid
316	3	10.3	38	2	A49165	pituitary adenylat
317	3	10.3	38	2	A61070	pituitary adenylat
318	3	10.3	38	2	PS0129	H-2 class I histoc
319	3	10.3	38	2	S50764	ribosomal protein
320	3	10.3	38	2	E72247	ribosomal protein
321	3	10.3	38	2	H83113	50S ribosomal prot
322	3	10.3	38	2	AG0028	50S ribosomal prot
323	3	10.3	38	2	D91149	50S ribosomal subu
324	3	10.3	38	2	AF1008	50S ribosomal chai
325	3	10.3	38	2	PH1920	annexin-like 40K p
326	3	10.3	38	2	S72344	pileE protein - Nei
327	3	10.3	38	2	A60216	hyperglycemic horm
328	3	10.3	38	2	S65416	pyruvate synthase
329	3	10.3	38	2	B95069	hypothetical prote
330	3	10.3	38	2	A95139	hypothetical prote
331	3	10.3	38	2	H91111	hypothetical prote
332	3	10.3	38	2	D90631	hypothetical prote
333	3	10.3	38	2	E72306	hypothetical prote
334	3	10.3	38	2	E81873	hypothetical prote
335	3	10.3	38	2	T14885	hypothetical prote
336	3	10.3	38	2	A82478	hypothetical prote
337	3	10.3	38	2	E82463	hypothetical prote
338	3	10.3	38	2	A82450	hypothetical prote
339	3	10.3	38	2	D37842	hypothetical prote
340	3	10.3	38	2	B69492	hypothetical prote
341	3	10.3	38	2	S23173	photosystem I chai
342	3	10.3	38	2	T01992	hypothetical prote
343	3	10.3	38	2	S58601	hypothetical prote
344	3	10.3	38	2	T01741	hypothetical prote
345	3	10.3	38	2	B39888	synapsin I - bovin
346	3	10.3	38	2	A83863	hypothetical prote
347	3	10.3	38	2	H81603	hypothetical prote
348	3	10.3	38	2	E82858	hypothetical prote
349	3	10.3	38	2	G71305	probable ribosomal
350	3	10.3	38	2	B97327	hypothetical prote
351	3	10.3	38	2	E86077	hypothetical prote
352	3	10.3	38	2	H85994	50S ribosomal subu
353	3	10.3	38	2	AB0747	hypothetical prote
354	3	10.3	38	2	AH0774	hypothetical prote
355	3	10.3	38	2	C97551	hypothetical prote

356	3	10.3	39	1	CTDFAS	corticotropin - sp
357	3	10.3	39	1	HWGH3Z	exendin-3 - Mexica
358	3	10.3	39	1	HWGH4G	exendin-4 - Gila m
359	3	10.3	39	2	B45946	gamma-glutamyltran
360	3	10.3	39	2	I55325	aspartate transami
361	3	10.3	39	2	S09645	hygromycin-B kinas
362	3	10.3	39	2	A01458	corticotropin - fi
363	3	10.3	39	2	PN0127	corticotropin - se
364	3	10.3	39	2	A61127	adrenocorticotropi
365	3	10.3	39	2	A01459	corticotropin - os
366	3	10.3	39	2	A01457	corticotropin - ra
367	3	10.3	39	2	C55995	prostaglandin E2 r
368	3	10.3	39	2	S07458	Ig kappa chain V r
369	3	10.3	39	2	PH0878	Ig kappa chain V r
370	3	10.3	39	2	S72459	ribosomal protein
371	3	10.3	39	2	PQ0011	tubulin beta chain
372	3	10.3	39	2	S63482	tubulin beta chain
373	3	10.3	39	2	A45793	actin - nematode (
374	3	10.3	39	2	AH2286	photosystem II pro
375	3	10.3	39	2	G64944	yebJ protein - Esc
376	3	10.3	39	2	A85795	hypothetical prote
377	3	10.3	39	2	S78008	fucosyltransferase
378	3	10.3	39	2	A48110	RNA recognition mo
379	3	10.3	39	2	H95146	hypothetical prote
380	3	10.3	39	2	D70239	hypothetical prote
381	3	10.3	39	2	C70254	hypothetical prote
382	3	10.3	39	2	G81899	hypothetical prote
383	3	10.3	39	2	B81912	hypothetical prote
384	3	10.3	39	2	B81954	very hypothetical
385	3	10.3	39	2	F82329	hypothetical prote
386	3	10.3	39	2	A43591	43K outer membrane
387	3	10.3	39	2	A44918	lactococcin G pept
388	3	10.3	39	2	S67938	hypothetical prote
389	3	10.3	39	2	S73118	photosystem II pro
390	3	10.3	39	2	PC4294	high mobility grou
391	3	10.3	39	2	T15158	hypothetical prote
392	3	10.3	39	2	I46466	luteinizing hormon
393	3	10.3	39	2	B40984	finger protein zfe
394	3	10.3	39	2	T03365	gene e2 protein -
395	3	10.3	39	2	F81587	hypothetical prote
396	3	10.3	39	2	E81540	hypothetical prote
397	3	10.3	39	2	T12905	hypothetical prote
398	3	10.3	39	2	AD0162	hypothetical prote
399	3	10.3	39	2	AE3109	hypothetical prote
400	3	10.3	40	1	SWFGS	sauvagine - Sauvag
401	3	10.3	40	2	B61320	plastocyanin - Aqu
402	3	10.3	40	2	S52343	hypothetical prote
403	3	10.3	40	2	S00264	creatine kinase (E
404	3	10.3	40	2	S34407	adenylate kinase (
405	3	10.3	40	2	PQ0202	endo-1,4-beta-xyla
406	3	10.3	40	2	S50021	trypsin-like prote
407	3	10.3	40	2	B60908	beta-lactamase (EC
408	3	10.3	40	2	B41440	protein disulfide-
409	3	10.3	40	2	A19940	antithrombin III -
410	3	10.3	40	2	B59005	thymosin beta - sc
411	3	10.3	40	2	A59005	thymosin beta - se
412	3	10.3	40	2	B31791	sarcotoxin ID - fl

413	3	10.3	40	2	S07969	T-cell receptor al
414	3	10.3	40	2	I50012	MHC class I protei
415	3	10.3	40	2	I50013	MHC class I protei
416	3	10.3	40	2	S61539	ribosomal protein
417	3	10.3	40	2	A60171	proteoglycan core
418	3	10.3	40	2	A60645	tubulin beta chain
419	3	10.3	40	2	A29184	vitellogenin - tur
420	3	10.3	40	2	S65907	conglutin gamma -
421	3	10.3	40	2	S08656	protein VI - human
422	3	10.3	40	2	A53708	indolepyruvate syn
423	3	10.3	40	2	T08107	nonenzymatic prote
424	3	10.3	40	2	S71917	hemoglobin, extrac
425	3	10.3	40	2	S58853	homeotic protein u
426	3	10.3	40	2	H95063	hypothetical prote
427	3	10.3	40	2	H91281	hypothetical prote
428	3	10.3	40	2	A87642	hypothetical prote
429	3	10.3	40	2	F87419	hypothetical prote
430	3	10.3	40	2	C32338	hypothetical 4K pr
431	3	10.3	40	2	C72398	hypothetical prote
432	3	10.3	40	2	S44935	hypothetical prote
433	3	10.3	40	2	A82203	hypothetical prote
434	3	10.3	40	2	A82382	hypothetical prote
435	3	10.3	40	2	I39944	regulatory extrace
436	3	10.3	40	2	F69677	phosphatase (RapK)
437	3	10.3	40	2	I41476	probable antigen 9
438	3	10.3	40	2	S27709	hypothetical prote
439	3	10.3	40	2	F45095	photosystem I ligh
440	3	10.3	40	2	T11811	hypothetical prote
441	3	10.3	40	2	T07472	hypothetical prote
442	3	10.3	40	2	T07516	hypothetical prote
443	3	10.3	40	2	T07523	hypothetical prote
444	3	10.3	40	2	T48629	hypothetical prote
445	3	10.3	40	2	S53001	mitotic-specific c
446	3	10.3	40	2	T03831	hypothetical prote
447	3	10.3	40	2	S71295	deoxyguanosine kin
448	3	10.3	40	2	S56768	capsid protein - L
449	3	10.3	40	2	T07206	hypothetical prote
450	3	10.3	40	2	H81592	hypothetical prote
451	3	10.3	40	2	H81520	hypothetical prote
452	3	10.3	40	2	F81511	hypothetical prote
453	3	10.3	40	2	G82620	hypothetical prote
454	3	10.3	40	2	A82590	hypothetical prote
455	3	10.3	40	2	A86123	hypothetical prote
456	3	10.3	40	2	B97413	hypothetical prote
457	2	6.9	28	1	LFSEW	trp operon leader
458	2	6.9	28	1	LFEBLT	leu operon leader
459	2	6.9	28	1	LFECL	leu operon leader
460	2	6.9	28	1	G9BPSV	gene 9 protein - s
461	2	6.9	28	2	S41774	ubiquinol-cytochro
462	2	6.9	28	2	S71598	cytochrome P450 HP
463	2	6.9	28	2	S04341	cytochrome P450 PB
464	2	6.9	28	2	PX0033	cytochrome P450 te
465	2	6.9	28	2	S66436	allophycocyanin al
466	2	6.9	28	2	S47624	D-aspartate oxidas
467	2	6.9	28	2	T14210	NADH2 dehydrogenas
468	2	6.9	28	2	T14213	NADH2 dehydrogenas
469	2	6.9	28	2	T12301	NADH2 dehydrogenas

470	2	6.9	28	2	PC1162	cytochrome-c oxida
471	2	6.9	28	2	S21278	glutathione transf
472	2	6.9	28	2	C33948	glutathione transf
473	2	6.9	28	2	A34244	hexokinase (EC 2.7
474	2	6.9	28	2	D38578	protein kinase 4 (
475	2	6.9	28	2	B39116	epidermal growth f
476	2	6.9	28	2	A31859	deoxycytidine kina
477	2	6.9	28	2	B54257	deoxynucleoside ki
478	2	6.9	28	2	I55596	lysosomal acid lip
479	2	6.9	28	2	B35948	phospholipase A2 (
480	2	6.9	28	2	C35948	phospholipase A2 (
481	2	6.9	28	2	A35115	hypothetical prote
482	2	6.9	28	2	A61281	lysozyme homolog A
483	2	6.9	28	2	A61529	chymotrypsin (EC 3
484	2	6.9	28	2	A60291	24K proteinase (EC
485	2	6.9	28	2	S08186	proteasome beta ch
486	2	6.9	28	2	S55729	orotidine-5'-monop
487	2	6.9	28	2	I40034	trpE protein - Bac
488	2	6.9	28	2	A32643	deoxyribodipyrimid
489	2	6.9	28	2	S77854	glutamate-tRNA lig
490	2	6.9	28	2	JX0059	serine proteinase
491	2	6.9	28	2	S07156	trypsin inhibitor
492	2	6.9	28	2	JX0058	trypsin inhibitor
493	2	6.9	28	2	B45041	trypsin inhibitor
494	2	6.9	28	2	S20393	trypsin inhibitor
495	2	6.9	28	2	A25802	2S seed storage pr
496	2	6.9	28	2	T47196	RAS protein [impor
497	2	6.9	28	2	A61322	somatostatin-28 -
498	2	6.9	28	2	B60583	glycoprotein hormo
499	2	6.9	28	2	A38232	vasoactive intesti
500	2	6.9	28	2	A60303	vasoactive intesti
501	2	6.9	28	2	JT0412	bombyxin-IV chain
502	2	6.9	28	2	A56366	intestinal trefoil
503	2	6.9	28	2	C44180	alpha-neurotoxin-l
504	2	6.9	28	2	C39327	long neurotoxin -
505	2	6.9	28	2	I32529	Ig lambda chain V
506	2	6.9	28	2	PC1001	Ig light chain V r
507	2	6.9	28	2	B47719	T-cell receptor al
508	2	6.9	28	2	D47719	T-cell receptor al
509	2	6.9	28	2	S58389	T-cell receptor be
510	2	6.9	28	2	PH0250	T-cell receptor Vb
511	2	6.9	28	2	PH0247	T-cell receptor Vb
512	2	6.9	28	2	A49829	T-cell receptor va
513	2	6.9	28	2	D49829	T-cell receptor va
514	2	6.9	28	2	PH1908	T-cell receptor al
515	2	6.9	28	2	D41912	T-cell receptor be
516	2	6.9	28	2	G47719	house-dust-mite-re
517	2	6.9	28	2	E49533	T-cell receptor be
518	2	6.9	28	2	I46921	gene Bota protein
519	2	6.9	28	2	S11618	ribosomal protein
520	2	6.9	28	2	S51060	ribosomal protein
521	2	6.9	28	2	S51067	ribosomal protein
522	2	6.9	28	2	S72460	ribosomal protein
523	2	6.9	28	2	S08569	ribosomal protein
524	2	6.9	28	2	S10052	ribosomal protein
525	2	6.9	28	2	S55442	beta A2 crystallin
526	2	6.9	28	2	A45626	beta 2-tubulin - n

527	2	6.9	28	2	S21231	calcium-binding pr
528	2	6.9	28	2	A23691	apolipoprotein C-I
529	2	6.9	28	2	A05296	fibrinogen alpha c
530	2	6.9	28	2	A61113	cellular retinol-b
531	2	6.9	28	2	B35577	cell adhesion rece
532	2	6.9	28	2	I48349	fibronectin - mous
533	2	6.9	28	2	A61233	retinol-binding pr
534	2	6.9	28	2	I45911	dnaK-type molecula
535	2	6.9	28	2	PQ0263	dnaK-type molecula
536	2	6.9	28	2	A03356	omega-gliadin - ei
537	2	6.9	28	2	A60359	pollen allergen DG
538	2	6.9	28	2	A60752	outer membrane pro
539	2	6.9	28	2	PQ0691	photosystem I 5.6K
540	2	6.9	28	2	G32351	34K class B flagel
541	2	6.9	28	2	S47614	zinc finger protei
542	2	6.9	28	2	S49924	stp protein (Baker
543	2	6.9	28	2	B39227	calcium channel pr
544	2	6.9	28	2	F54346	pyruvate synthase
545	2	6.9	28	2	A36153	major allergen Ole
546	2	6.9	28	2	B54127	dolichyl-diphospho
547	2	6.9	28	2	S56746	alpha-synuclein, N
548	2	6.9	28	2	I48178	orphan receptor -
549	2	6.9	28	2	PC4429	peroxisome prolife
550	2	6.9	28	2	PC4430	peroxisome prolife
551	2	6.9	28	2	S29135	aminopyrine N-deme
552	2	6.9	28	2	S29136	aminopyrine N-deme
553	2	6.9	28	2	PN0625	homeobox JRX prote
554	2	6.9	28	2	B56779	tetM 5'-region lea
555	2	6.9	28	2	JU0297	fruR-shl operon le
556	2	6.9	28	2	G90638	leu operon leader
557	2	6.9	28	2	C90639	fruR leader peptid
558	2	6.9	28	2	B47310	MHVS28AA - murine
559	2	6.9	28	2	E64656	hypothetical prote
560	2	6.9	28	2	B64669	hypothetical prote
561	2	6.9	28	2	S15235	hypothetical prote
562	2	6.9	28	2	C56262	uvrB 3'-region hyp
563	2	6.9	28	2	E81239	hypothetical prote
564	2	6.9	28	2	I60364	phosphorybosylpyro
565	2	6.9	28	2	S56121	type I DNA methylt
566	2	6.9	28	2	B39191	hypothetical prote
567	2	6.9	28	2	T17391	hypothetical prote
568	2	6.9	28	2	A56499	brevicin-27 - Lact
569	2	6.9	28	2	A41476	probable antigen 1
570	2	6.9	28	2	S16228	aryl acylamidase -
571	2	6.9	28	2	G69384	conserved hypothet
572	2	6.9	28	2	A69259	hypothetical prote
573	2	6.9	28	2	T06925	hypothetical prote
574	2	6.9	28	2	S38524	rRNA N-glycosidase
575	2	6.9	28	2	PQ0800	calmodulin antagon
576	2	6.9	28	2	T06340	ribosomal protein
577	2	6.9	28	2	T07599	hypothetical prote
578	2	6.9	28	2	PH0220	peroxidase (EC 1.1
579	2	6.9	28	2	JQ0272	hypothetical 3K pr
580	2	6.9	28	2	S46250	fatty-acid-binding
581	2	6.9	28	2	A44923	carboxypeptidase 3
582	2	6.9	28	2	S64701	hypothetical prote
583	2	6.9	28	2	T38041	similarity to yeas

584	2	6.9	28	2	A27261	proteinase inhibit
585	2	6.9	28	2	A61417	bdellin B-3 - medi
586	2	6.9	28	2	S06668	toxin-like protein
587	2	6.9	28	2	S07826	venom protein - Am
588	2	6.9	28	2	C34923	omega-agatoxin IIA
589	2	6.9	28	2	A44877	cell surface prote
590	2	6.9	28	2	JW0019	mast cell degranul
591	2	6.9	28	2	A61273	interleukin-1 - st
592	2	6.9	28	2	S68643	nicotinic acetylch
593	2	6.9	28	2	PC2162	angiotensin II rec
594	2	6.9	28	2	I54183	cell adhesion regu
595	2	6.9	28	2	S54338	cytochrome P450 CY
596	2	6.9	28	2	I52627	erythrocyte chemok
597	2	6.9	28	2	JQ1035	hypothetical 3.2K
598	2	6.9	28	2	PH1335	Ig heavy chain DJ
599	2	6.9	28	2	S37683	protein IEF SSP 91
600	2	6.9	28	2	S37686	protein IEF SSP 92
601	2	6.9	28	2	PH1911	T-cell receptor al
602	2	6.9	28	2	I39288	ZF3 domain - human
603	2	6.9	28	2	PL0005	pepsin A (EC 3.4.2
604	2	6.9	28	2	A60692	proline-rich prote
605	2	6.9	28	2	PC2239	heat shock protein
606	2	6.9	28	2	PT0366	T-cell receptor be
607	2	6.9	28	2	I58115	cystic fibrosis tr
608	2	6.9	28	2	A46690	sialic acid-specif
609	2	6.9	28	2	C83797	hypothetical prote
610	2	6.9	28	2	C83969	hypothetical prote
611	2	6.9	28	2	S51593	myrB protein - Mic
612	2	6.9	28	2	C85490	fruR leader peptid
613	2	6.9	28	2	C97078	hypothetical prote
614	2	6.9	28	2	F97000	hypothetical prote
615	2	6.9	28	2	G85489	leu operon leader
616	2	6.9	28	2	H85908	hypothetical prote
617	2	6.9	28	2	AB1093	hypothetical prote
618	2	6.9	28	2	T06490	probable ribulose-
619	2	6.9	28	2	S73563	H+-transporting tw
620	2	6.9	28	2	AG0516	leu operon leader
621	2	6.9	28	4	I68614	frame shifted FMR1
622	2	6.9	28	4	JN0014	GABA(A) receptor a
623	2	6.9	29	1	TIPU	trypsin inhibitor
624	2	6.9	29	1	TIPU3	trypsin inhibitor
625	2	6.9	29	1	TIPU2B	trypsin inhibitor
626	2	6.9	29	1	GCOPV	glucagon - North A
627	2	6.9	29	1	GCDK	glucagon - duck
628	2	6.9	29	1	A61583	glucagon - ostrich
629	2	6.9	29	1	GCFLE	glucagon - Europea
630	2	6.9	29	1	GCDF	glucagon - smaller
631	2	6.9	29	1	GCEN	glucagon - elephan
632	2	6.9	29	1	GCTTS	glucagon - slider
633	2	6.9	29	1	TNLJBR	trans-activating t
634	2	6.9	29	1	Q1BP57	gene 1.5 protein -
635	2	6.9	29	2	A60558	cytochrome P450 HL
636	2	6.9	29	2	T17079	NADH2 dehydrogenas
637	2	6.9	29	2	T17076	NADH2 dehydrogenas
638	2	6.9	29	2	A48427	flavohemoglobin hm
639	2	6.9	29	2	A54234	cytochrome-c oxida
640	2	6.9	29	2	S08201	peroxidase (EC 1.1

641	2	6.9	29	2	A26208	acetyl-CoA C-acety
642	2	6.9	29	2	A22018	phosphotransferase
643	2	6.9	29	2	S46211	kallikrein rK8 (pK
644	2	6.9	29	2	S28174	heat-shock protein
645	2	6.9	29	2	A32414	bothrolysin (EC 3.
646	2	6.9	29	2	S17432	H+-transporting tw
647	2	6.9	29	2	S02578	H+-transporting tw
648	2	6.9	29	2	S23122	peptidylprolyl iso
649	2	6.9	29	2	JU0211	squash-type trypsi
650	2	6.9	29	2	T03653	phospholipid trans
651	2	6.9	29	2	C24536	alpha-amylase/tryp
652	2	6.9	29	2	C25310	alpha-amylase/tryp
653	2	6.9	29	2	D55998	brevinin-2Ed - edi
654	2	6.9	29	2	D53578	brevinin-2Ee - edi
655	2	6.9	29	2	A91740	glucagon - turkey
656	2	6.9	29	2	A91741	glucagon - rabbit
657	2	6.9	29	2	A91742	glucagon - Arabian
658	2	6.9	29	2	S07211	glucagon - marbled
659	2	6.9	29	2	A61135	glucagon - bigeye
660	2	6.9	29	2	C39258	glucagon - common
661	2	6.9	29	2	C60840	glucagon I - Europ
662	2	6.9	29	2	S39018	glucagon - bowfin
663	2	6.9	29	2	A39462	cholestinin - do
664	2	6.9	29	2	A60791	toxin II.9 - scorp
665	2	6.9	29	2	JH0699	omega-conotoxin MV
666	2	6.9	29	2	A58537	omega-conotoxin MV
667	2	6.9	29	2	I52628	low affinity nerve
668	2	6.9	29	2	C61233	conceptus protein
669	2	6.9	29	2	S10061	Ig heavy chain (cl
670	2	6.9	29	2	PH0239	T-cell receptor Vb
671	2	6.9	29	2	PH0251	T-cell receptor Vb
672	2	6.9	29	2	PH0254	T-cell receptor Vb
673	2	6.9	29	2	PH0233	T-cell receptor Vb
674	2	6.9	29	2	E31485	Ig heavy chain V r
675	2	6.9	29	2	H31485	Ig kappa chain V r
676	2	6.9	29	2	G31461	T-cell receptor de
677	2	6.9	29	2	C47719	T-cell receptor al
678	2	6.9	29	2	E47719	house-dust-mite-re
679	2	6.9	29	2	PS0134	H-2 class I histoc
680	2	6.9	29	2	PS0132	H-2 class I histoc
681	2	6.9	29	2	I37534	gene HLA-DRB prote
682	2	6.9	29	2	I37535	gene HLA-DRB prote
683	2	6.9	29	2	I37536	MHC class II histo
684	2	6.9	29	2	I37301	MHC class II histo
685	2	6.9	29	2	I37303	HLA-DR beta - huma
686	2	6.9	29	2	I37306	HLA-DR beta - huma
687	2	6.9	29	2	I50214	protein-tyrosine-p
688	2	6.9	29	2	S07771	histone H2B.2, spe
689	2	6.9	29	2	T04412	histone H3 - barle
690	2	6.9	29	2	S51070	ribosomal protein
691	2	6.9	29	2	S08555	ribosomal protein
692	2	6.9	29	2	PC4231	ribosomal protein
693	2	6.9	29	2	S10050	ribosomal protein
694	2	6.9	29	2	S10049	ribosomal protein
695	2	6.9	29	2	S26229	ribosomal protein
696	2	6.9	29	2	A27561	Meth A tumor-speci
697	2	6.9	29	2	S10725	calmodulin-binding

698	2	6.9	29	2	B44101	calmodulin, vasoac
699	2	6.9	29	2	E33208	calreticulin, uter
700	2	6.9	29	2	C33208	calreticulin, slow
701	2	6.9	29	2	D33208	calreticulin, brai
702	2	6.9	29	2	A45474	thrombospondin 2 -
703	2	6.9	29	2	G39690	neural cell adhesi
704	2	6.9	29	2	A61166	endometrial proges
705	2	6.9	29	2	I52402	alpha-fetoprotein
706	2	6.9	29	2	S57232	homeotic protein s
707	2	6.9	29	2	S06854	chorion class B pr
708	2	6.9	29	2	A43038	auxin-binding prot
709	2	6.9	29	2	T12082	proline-rich prote
710	2	6.9	29	2	S70328	gamma35 secalin -
711	2	6.9	29	2	S29208	avenin gamma-3 - o
712	2	6.9	29	2	S07055	photosystem I prot
713	2	6.9	29	2	S05032	photosystem II pro
714	2	6.9	29	2	S08088	gene VII protein -
715	2	6.9	29	2	F42075	finger protein (cl
716	2	6.9	29	2	S42642	probable rhicadhes
717	2	6.9	29	2	T51116	probable precorrin
718	2	6.9	29	2	A53145	high conductance c
719	2	6.9	29	2	A35121	hypothetical prote
720	2	6.9	29	2	S03277	photosystem II 5K
721	2	6.9	29	2	A55891	delta-conotoxin Gm
722	2	6.9	29	2	S32730	homeotic protein -
723	2	6.9	29	2	S57225	labial protein (cl
724	2	6.9	29	2	S32732	homeotic protein -
725	2	6.9	29	2	S32734	homeotic protein -
726	2	6.9	29	2	S32733	homeotic protein -
727	2	6.9	29	2	G90719	hypothetical prote
728	2	6.9	29	2	S07513	gene 5.1 protein -
729	2	6.9	29	2	S14040	hypothetical prote
730	2	6.9	29	2	E64586	hypothetical prote
731	2	6.9	29	2	B64607	hypothetical prote
732	2	6.9	29	2	G64674	hypothetical prote
733	2	6.9	29	2	G83440	KdpF protein PA163
734	2	6.9	29	2	A49288	alcohol dehydrogen
735	2	6.9	29	2	A81078	hypothetical prote
736	2	6.9	29	2	B81006	hypothetical prote
737	2	6.9	29	2	T48910	KdpF protein [vali
738	2	6.9	29	2	A35445	repY protein - Esc
739	2	6.9	29	2	S19943	aadB protein - Kle
740	2	6.9	29	2	A49914	S-layer protein va
741	2	6.9	29	2	E64036	hypothetical prote
742	2	6.9	29	2	B48363	2-hydroxyglutaryl-
743	2	6.9	29	2	C40638	orf 3' of cycI - R
744	2	6.9	29	2	B56817	photosystem I chai
745	2	6.9	29	2	S74572	hypothetical prote
746	2	6.9	29	2	C60743	putrescine carbamo
747	2	6.9	29	2	S67989	HA-19/HA-52 protei
748	2	6.9	29	2	S14099	12-alpha-hydroxyst
749	2	6.9	29	2	S77569	plantaricin SA6 -
750	2	6.9	29	2	S21222	48K protein - Euba
751	2	6.9	29	2	S03947	hydrogen dehydroge
752	2	6.9	29	2	T37120	hypothetical prote
753	2	6.9	29	2	T36654	probable small mem
754	2	6.9	29	2	B43937	endo-1,4-beta-xyla

755	2	6.9	29	2	S09556	hypothetical prote
756	2	6.9	29	2	T06904	hypothetical prote
757	2	6.9	29	2	S73197	hypothetical prote
758	2	6.9	29	2	S78326	conserved hypothet
759	2	6.9	29	2	S78310	hypothetical prote
760	2	6.9	29	2	S78360	hypothetical prote
761	2	6.9	29	2	S01572	hypothetical prote
762	2	6.9	29	2	T07450	hypothetical prote
763	2	6.9	29	2	S01448	hypothetical prote
764	2	6.9	29	2	S38525	rRNA N-glycosidase
765	2	6.9	29	2	T52557	translation elonga
766	2	6.9	29	2	PQ0862	allantoinase (EC 3
767	2	6.9	29	2	PQ0486	globulin 2a - taro
768	2	6.9	29	2	S02200	prolamin alpha-1 -
769	2	6.9	29	2	A60683	malate dehydrogena
770	2	6.9	29	2	JQ0212	hypothetical 3K pr
771	2	6.9	29	2	S58541	hypothetical prote
772	2	6.9	29	2	PC2035	alanine transamina
773	2	6.9	29	2	S78714	protein YDR524w-a
774	2	6.9	29	2	B21112	variant surface gl
775	2	6.9	29	2	C60110	repetitive protein
776	2	6.9	29	2	D24802	cuticle protein 36
777	2	6.9	29	2	A56591	E75 steroid recept
778	2	6.9	29	2	A61613	ceratotoxin A - Me
779	2	6.9	29	2	B61613	ceratotoxin B - Me
780	2	6.9	29	2	PH1230	lectin - namazu (f
781	2	6.9	29	2	A32860	biotin-binding pro
782	2	6.9	29	2	I50382	c-mil protein - ch
783	2	6.9	29	2	I50695	non-collagenous al
784	2	6.9	29	2	B54197	70k thyroid autoan
785	2	6.9	29	2	A35891	carcinoembryonic a
786	2	6.9	29	2	I77372	CD44SP - human
787	2	6.9	29	2	S54340	diazepam binding i
788	2	6.9	29	2	A41683	hyaluronate recept
789	2	6.9	29	2	C54037	splicing regulator
790	2	6.9	29	2	S35924	T-cell receptor ga
791	2	6.9	29	2	C61384	trachael mucin gly
792	2	6.9	29	2	A60604	glutathione peroxi
793	2	6.9	29	2	S57204	oviduct-specific s
794	2	6.9	29	2	I47025	antigen WC1 [impor
795	2	6.9	29	2	A49410	t-complex polypept
796	2	6.9	29	2	PS0125	H-2 class I histoc
797	2	6.9	29	2	S46929	tegl69 protein - m
798	2	6.9	29	2	S38749	vimentin homolog -
799	2	6.9	29	2	S42764	Ca2+/calmodulin-de
800	2	6.9	29	2	A49708	synaptosomal-assoc
801	2	6.9	29	2	H83777	hypothetical prote
802	2	6.9	29	2	C83833	hypothetical prote
803	2	6.9	29	2	F83870	hypothetical prote
804	2	6.9	29	2	B84144	hypothetical prote
805	2	6.9	29	2	PC4421	multactivase (EC 3
806	2	6.9	29	2	B85840	hypothetical prote
807	2	6.9	29	2	C85840	hypothetical prote
808	2	6.9	29	2	G86058	hypothetical prote
809	2	6.9	29	2	E89904	hypothetical prote
810	2	6.9	29	2	H89949	hypothetical prote
811	2	6.9	29	2	A59278	neurotoxin BmK A3-

812	2	6.9	29	2	S17496	inorganic diphosph
813	2	6.9	29	2	PQ0782	NADH2 dehydrogenas
814	2	6.9	29	2	S34762	L-serine ammonia-l
815	2	6.9	29	2	AB0717	hypothetical prote
816	2	6.9	29	2	AC0717	hypothetical prote
817	2	6.9	29	2	AH2338	PetN protein [impo
818	2	6.9	29	4	I58970	hypothetical prote
819	2	6.9	30	1	AIBSAF	thermophilic amino
820	2	6.9	30	1	TIPU1W	trypsin inhibitor
821	2	6.9	30	1	OEON2K	beta-endorphin II
822	2	6.9	30	1	IRTRC3	protamine CIII, ma
823	2	6.9	30	1	IRTRC2	protamine Ia - rai
824	2	6.9	30	1	IRTR78	protamine CIII, mi
825	2	6.9	30	1	IRTR4	protamine pTP4 - r
826	2	6.9	30	1	CLHRY2	protamine VII - Pa
827	2	6.9	30	1	CLHR2A	protamine VII - At
828	2	6.9	30	1	SNUMP	sillucin - Rhizomu
829	2	6.9	30	2	I57689	ubiquinol-cytochro
830	2	6.9	30	2	I52254	gene CYP11B2 prote
831	2	6.9	30	2	B56859	fatty acid omega-h
832	2	6.9	30	2	A27375	photosystem I iron
833	2	6.9	30	2	S11131	NADH2 dehydrogenas
834	2	6.9	30	2	S14214	NADH2 dehydrogenas
835	2	6.9	30	2	S08202	peroxidase (EC 1.1
836	2	6.9	30	2	S08204	peroxidase (EC 1.1
837	2	6.9	30	2	S08203	peroxidase (EC 1.1
838	2	6.9	30	2	A39089	hydrogenase (EC 1.
839	2	6.9	30	2	I38066	nitric-oxide synth
840	2	6.9	30	2	I39799	CAT-66 - Bacillus
841	2	6.9	30	2	A18780	dimethylallyltrans
842	2	6.9	30	2	S03283	methionine adenosy
843	2	6.9	30	2	S71865	glutathione transf
844	2	6.9	30	2	B27103	aspartate transami
845	2	6.9	30	2	A27103	aspartate transami
846	2	6.9	30	2	I55427	aspartate transami
847	2	6.9	30	2	A49955	protein-tyrosine k
848	2	6.9	30	2	S68639	nigroxin A - black
849	2	6.9	30	2	S68640	nigroxin B - black
850	2	6.9	30	2	A05004	pancreatic ribonuc
851	2	6.9	30	2	D57001	endo-1,4-beta-xyla
852	2	6.9	30	2	A43937	endo-1,4-beta-xyla
853	2	6.9	30	2	PC2361	alpha-glucosidase
854	2	6.9	30	2	PX0073	epoxide hydrolase
855	2	6.9	30	2	B60291	30K serine protein
856	2	6.9	30	2	A27634	major fecal allerg
857	2	6.9	30	2	B27634	major fecal allerg
858	2	6.9	30	2	I77411	renin-2 - mouse (f
859	2	6.9	30	2	PC2328	proteasome endopep
860	2	6.9	30	2	A34486	inorganic diphosph
861	2	6.9	30	2	S21816	H+-exporting ATPas
862	2	6.9	30	2	S21814	H+-exporting ATPas
863	2	6.9	30	2	S74121	fructose-bisphosph
864	2	6.9	30	2	S25666	phosphopyruvate hy
865	2	6.9	30	2	S69600	peptidylprolyl iso
866	2	6.9	30	2	A60517	alpha-1-antitrypsi
867	2	6.9	30	2	S24979	proteinase inhibit
868	2	6.9	30	2	JX0057	trypsin inhibitor

869	2	6.9	30	2	JS0579	squash-type trypsi
870	2	6.9	30	2	JQ1958	trypsin inhibitor
871	2	6.9	30	2	PC1113	proteinase inhibit
872	2	6.9	30	2	C42842	antifungal 2S stor
873	2	6.9	30	2	S70341	napin large chain
874	2	6.9	30	2	S70343	napin large chain
875	2	6.9	30	2	A33308	thrombomodulin - r
876	2	6.9	30	2	S01657	atrial natriuretic
877	2	6.9	30	2	A61130	somatotropin - Ame
878	2	6.9	30	2	S44473	glucagon-like pept
879	2	6.9	30	2	B61125	glucagon-like pept
880	2	6.9	30	2	C61125	glucagon-like pept
881	2	6.9	30	2	A59076	defensin alpha-1 -
882	2	6.9	30	2	B59076	defensin alpha-2 -
883	2	6.9	30	2	C59076	defensin alpha-3 -
884	2	6.9	30	2	B60791	toxin II.6 - scorp
885	2	6.9	30	2	A31187	neurotoxin II.22.5
886	2	6.9	30	2	I68109	interferon alpha-W
887	2	6.9	30	2	C49533	T-cell receptor al
888	2	6.9	30	2	S20778	Ig heavy chain V r
889	2	6.9	30	2	PL0092	Ig heavy chain V r
890	2	6.9	30	2	PH0245	T-cell receptor Vb
891	2	6.9	30	2	PH0228	T-cell receptor Vb
892	2	6.9	30	2	PH0252	T-cell receptor Vb
893	2	6.9	30	2	PH0882	Ig kappa chain V r
894	2	6.9	30	2	E31461	T-cell receptor de
895	2	6.9	30	2	PH0235	T-cell receptor Vb
896	2	6.9	30	2	A49533	T-cell receptor al
897	2	6.9	30	2	C27579	T-cell receptor be
898	2	6.9	30	2	I37626	Fc gamma (IgG) rec
899	2	6.9	30	2	PS0121	H-2 class I histoc
900	2	6.9	30	2	S74192	crotoxin inhibitor
901	2	6.9	30	2	A05253	hemoglobin epsilon
902	2	6.9	30	2	A21680	hemoglobin epsilon
903	2	6.9	30	2	A05254	hemoglobin epsilon
904	2	6.9	30	2	S68618	histone H2B - sea
905	2	6.9	30	2	PD0014	cAMP response elem
906	2	6.9	30	2	S11613	ribosomal protein
907	2	6.9	30	2	S11617	ribosomal protein
908	2	6.9	30	2	A60511	gamma-crystallin -
909	2	6.9	30	2	I49412	gamma-crystallin-3
910	2	6.9	30	2	S12965	gamma-crystallin -
911	2	6.9	30	2	S69269	ezzrin homolog - bo
912	2	6.9	30	2	A61189	tubulin beta chain
913	2	6.9	30	2	I52806	Duchenne muscular
914	2	6.9	30	2	PC4172	profilin - rat (fr
915	2	6.9	30	2	S21153	calcium-binding pr
916	2	6.9	30	2	A26188	lipocortin I - pig
917	2	6.9	30	2	A56790	annexin, isoform P
918	2	6.9	30	2	A34622	fibrinogen beta ch
919	2	6.9	30	2	A03148	retinol-binding pr
920	2	6.9	30	2	A48299	taurine transporte
921	2	6.9	30	2	B61511	serum albumin, mil
922	2	6.9	30	2	B39819	neutrophil chemota
923	2	6.9	30	2	A38933	vitronectin - bovi
924	2	6.9	30	2	S57234	fushi tarazu segme
925	2	6.9	30	2	S69124	rRNA N-glycosidase

926	2	6.9	30	2	S69125	rRNA N-glycosidase
927	2	6.9	30	2	S07065	rRNA N-glycosidase
928	2	6.9	30	2	A31836	17K antigen - Rick
929	2	6.9	30	2	PQ0669	photosystem I 17.5
930	2	6.9	30	2	E45095	photosystem I ligh
931	2	6.9	30	2	B45095	photosystem I ligh
932	2	6.9	30	2	S30757	genome polyprotein
933	2	6.9	30	2	S30760	genome polyprotein
934	2	6.9	30	2	S30759	genome polyprotein
935	2	6.9	30	2	B44314	intracisternal A p
936	2	6.9	30	2	S26175	tail tubular prote
937	2	6.9	30	2	S69352	N-methylhydantoin
938	2	6.9	30	2	S68312	glucuronosyltransf
939	2	6.9	30	2	S42364	aromatic-amino-aci
940	2	6.9	30	2	S05223	photosystem I 6.5K
941	2	6.9	30	2	S28991	antifungal protein
942	2	6.9	30	2	PC2307	X-Pro aminopeptida
943	2	6.9	30	2	PQ0484	globulin lb - taro
944	2	6.9	30	2	C43591	51K outer membrane
945	2	6.9	30	2	B43591	45K outer membrane
946	2	6.9	30	2	S06411	killer plasmid 28K
947	2	6.9	30	2	B49292	GDP dissociation i
948	2	6.9	30	2	A60914	pheromone-binding
949	2	6.9	30	2	PS0437	potassium channel
950	2	6.9	30	2	PS0438	potassium channel
951	2	6.9	30	2	A47607	immunogenic protei
952	2	6.9	30	2	S02088	blood group Rh-rel
953	2	6.9	30	2	S29138	aniline monooxygen
954	2	6.9	30	2	S57227	proboscipedia prot
955	2	6.9	30	2	B95020	hypothetical prote
956	2	6.9	30	2	C95030	hypothetical prote
957	2	6.9	30	2	G95031	hypothetical prote
958	2	6.9	30	2	E95079	hypothetical prote
959	2	6.9	30	2	F95118	hypothetical prote
960	2	6.9	30	2	E95145	hypothetical prote
961	2	6.9	30	2	F89406	protein R10E8.7 [i
962	2	6.9	30	2	F87254	hypothetical prote
963	2	6.9	30	2	E84786	hypothetical prote
964	2	6.9	30	2	C84481	hypothetical prote
965	2	6.9	30	2	B47483	cysteine-rich para
966	2	6.9	30	2	S15141	hypothetical prote
967	2	6.9	30	2	S13985	hypothetical prote
968	2	6.9	30	2	S14038	hypothetical prote
969	2	6.9	30	2	S13994	hypothetical prote
970	2	6.9	30	2	A72205	hypothetical prote
971	2	6.9	30	2	E72356	hypothetical prote
972	2	6.9	30	2	H72312	hypothetical prote
973	2	6.9	30	2	S66448	trimethylamine deh
974	2	6.9	30	2	A70105	conserved hypothet
975	2	6.9	30	2	F70118	hypothetical prote
976	2	6.9	30	2	D70144	hypothetical prote
977	2	6.9	30	2	H70152	hypothetical prote
978	2	6.9	30	2	A70209	hypothetical prote
979	2	6.9	30	2	E70246	hypothetical prote
980	2	6.9	30	2	F70253	hypothetical prote
981	2	6.9	30	2	F70254	hypothetical prote
982	2	6.9	30	2	H64522	hypothetical prote

983	2	6.9	30	2	E64565	hypothetical prote
984	2	6.9	30	2	E64577	hypothetical prote
985	2	6.9	30	2	C64709	hypothetical prote
986	2	6.9	30	2	A83556	hypothetical prote
987	2	6.9	30	2	S30347	4-hydroxybenzoyl-C
988	2	6.9	30	2	PC2251	D-tagatose 3-epime
989	2	6.9	30	2	A44807	ethylene-forming e
990	2	6.9	30	2	S06966	hypothetical prote
991	2	6.9	30	2	S74107	cytochrome c' - Me
992	2	6.9	30	2	B81889	hypothetical prote
993	2	6.9	30	2	B81891	hypothetical prote
994	2	6.9	30	2	H81862	hypothetical prote
995	2	6.9	30	2	C81791	hypothetical prote
996	2	6.9	30	2	H81202	hypothetical prote
997	2	6.9	30	2	G81031	hypothetical prote
998	2	6.9	30	2	I69492	gene aeg-46.5 prot
999	2	6.9	30	2	A36733	hypothetical prote
1000	2	6.9	30	2	A60283	shiga-like toxin I

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 17.2%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	24	LRKKL	28
Db	26	LRKKL	30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 17.2%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||
Db 30 SVSEI 34

RESULT 3

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.
submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 13.8%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
||||
Db 15 LRKK 18

RESULT 4

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;
Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.

J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of
mutants of Methylobacterium extorquens AML unable to synthesize pyrroloquinoline
quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-29 <MOR>

A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590

C;Genetics:

A;Gene: pqqD

C;Superfamily: pyrroloquinoline quinone precursor pqqA

C;Keywords: quinoprotein

F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>

F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 13.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
||||
Db 8 VSEI 11

RESULT 5

I78537

copper transporting P-type ATPase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I78537

R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.
Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 13.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 6

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10, 'XXP', 14-15, 'X', 17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 13.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 7

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.

Eur. J. Biochem. 233, 800-808, 1995

A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate dehydrogenase genes from the thermophilic archaeon Sulfolobus solfataricus overlap by 8-bp: isolation, sequencing of the genes and expression in Escherichia coli.

A;Reference number: S63528; MUID:96085144; PMID:8521845

A;Accession: S63531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-30 <JON>

A;Cross-references: EMBL:X80178

Query Match 13.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
||||
Db 11 WLRK 14

RESULT 8

S44471

glucagon G1 - North American paddlefish (Polyodon spathula)

C;Species: Polyodon spathula

C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999

C;Accession: S44471

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44471

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Experimental source: pancreas

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 13.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
||||
Db 23 VEWL 26

RESULT 9

S44472

glucagon G2 - North American paddlefish (Polyodon spathula)

C;Species: Polyodon spathula

C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999

C;Accession: S44472

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 13.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
|||
Db 23 VEWL 26

RESULT 10

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Wathney, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058;

TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 13.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 26 KKLQ 29

RESULT 11

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: *Dendrocygna bicolor* (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 13.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 12

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 13.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
|||
Db 8 MERV 11

RESULT 13

E81714

hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

C;Accession: E81714

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;

Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;

Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,

W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,

C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81714

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <TET>
A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;
PID:g7190379; GSPDB:GN00121; TIGR:TC0337
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0337

Query Match 13.8%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 26 LRKK 29

RESULT 14

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 13.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 15

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 13.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 16

E95098

hypothetical protein SP0853 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0853

Query Match 13.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 30 KKLQ 33

RESULT 17

D82125

hypothetical protein VC2034 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill,

S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match 13.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 24 KKLQ 27

RESULT 18

S70806

hypothetical protein 5 - *Vibrio cholerae* (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: *Vibrio cholerae*

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 13.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20
 ||||
Db 14 SMER 17

RESULT 19

F95057
hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: F95057
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf, E.; Khouiri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0497

Query Match 13.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 10 KKLQ 13

RESULT 20

A84774
hypothetical protein At2g35870 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84774
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g35870
A;Map position: 2

Query Match 13.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 4 KKLQ 7

RESULT 21

S46227

hypothetical protein - Streptomyces chrysomallus (fragment)

C;Species: Streptomyces chrysomallus

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 13.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 22

S71912

hemoglobin, extracellular, chain A1 - polychaete (Perinereis aibuhitensis) (fragment)

C;Species: Perinereis aibuhitensis

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete Perinereis aibuhitensis.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology
C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 13.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 25 ERVE 28

RESULT 23

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: Helianthus annuus (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 13.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
|||
Db 6 RKKL 9

RESULT 24

CKFHCS

sarcotoxin IC - flesh fly (Sarcophaga peregrina)

C;Species: Sarcophaga peregrina

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997

A;Accession: C22625

A;Molecule type: protein

A;Residues: 1-39 <OKA>

C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial; hemolymph

F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 13.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 2 WLRK 5

RESULT 25

S71913

hemoglobin, extracellular, chain A2 - polychaete (*Perinereis aibuhitensis*)
(fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.;
Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the
polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71913

A;Molecule type: protein

A;Residues: 1-39 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 13.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 26

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: *Squalus acanthias* (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium
chloride transporting epithelia of the spiny dogfish, *Squalus acanthias*.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <PRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
|||
Db 10 KKL 12

RESULT 27

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake
(fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin
phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black
snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQL 7
|||
Db 3 IQL 5

RESULT 28

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human
sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 29

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 30

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999

C;Accession: S58386

R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.

Nucleic Acids Res. 23, 3074-3075, 1995

A;Title: A novel method for sequencing members of multi-gene families.

A;Reference number: S58384; MUID:95388532; PMID:7659534

A;Accession: S58386

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-28 <JOH>

A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

A;Note: only a part of the coding sequence is given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 10.3%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
|||
Db 12 ERV 14

RESULT 31

PN0047

signal transduction protein QM0017 - mouse (fragments)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 15-Oct-1999

C;Accession: PN0047

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0047

A;Molecule type: protein

A;Residues: 1-28 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.

C;Superfamily: signal transduction protein DJ-1

C;Keywords: brain

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 14 NLG 16

RESULT 32

S70894

hypothetical protein 1 - Vibrio anguillarum (fragment)

C;Species: Vibrio anguillarum

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S70894

R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.

Mol. Microbiol. 19, 625-637, 1996

A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen Vibrio anguillarum.

A;Reference number: S70894; MUID:96228710; PMID:8830252

A;Accession: S70894

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <OTO>

A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1;

PID:g1723992

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 33

S22469

hypothetical protein 1 - Prochlorothrix hollandica

C;Species: Prochlorothrix hollandica

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C;Accession: S22469; S16850

R;Greer, K.L.; Golden, S.S.

Plant Mol. Biol. 19, 355-365, 1992

A;Title: Conserved relationship between psbH and petBD genes: presence of a shared upstream element in Prochlorothrix hollandica.

A;Reference number: S22469; MUID:92322967; PMID:1623188

A;Accession: S22469

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <GRE>

A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 10.3%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
|||
Db 4 SVS 6

RESULT 34

S26254

rel protein - chicken

C;Species: Gallus gallus (chicken)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Dec-1996

C;Accession: S26254

R;Capobianco, A.J.; Gilmore, T.D.

Oncogene 6, 2203-2210, 1991

A;Title: Repression of the chicken c-rel promoter by vRel in chicken embryo fibroblasts is not mediated through a consensus NF-kappaB binding site.

A;Reference number: S26254; MUID:92115319; PMID:1766669

A;Accession: S26254

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-28 <CAP>

A;Cross-references: EMBL:X59588

Query Match 10.3%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22
|||
Db 1 RVE 3

RESULT 35

I59477

antigen, T-cell receptor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C;Accession: I59477

R;Mathioudakis, G.; Chen, P.

Scand. J. Immunol. 38, 31-36, 1993

A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the T-cell antigen receptor to J gamma 2C gamma 2 gene segments in peripheral blood lymphocyte transcripts from normal donors.

A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:g181658

C;Keywords: T-cell receptor

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28

|||

Db 10 KKL 12

RESULT 36

F46522

T-cell receptor eta chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: F46522; I56191

R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Weissman, A.M.

J. Immunol. 150, 122-130, 1993

A;Title: T cell antigen receptor-eta subunit. Low levels of expression and limited cross-species conservation.

A;Reference number: A46522; MUID:93107707; PMID:8417118

A;Accession: F46522

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-28 <JEN>

A;Cross-references: GB:S51404; NID:g262180; PIDN:AAB24606.1; PID:g262181

A;Note: sequence extracted from NCBI backbone (NCBIP:120909)

R;Itoh, Y.; Matsuura, A.; Kinebuchi, M.; Honda, R.; Takayama, S.; Ichimiya, S.; Kon, S.; Kikuchi, K.

J. Immunol. 151, 4705-4717, 1993

A;Title: Structural analysis of the CD3 zeta/eta locus of the rat. Expression of zeta but eta transcripts by rat T cells.

A;Reference number: I56191; MUID:94014415; PMID:8409430

A;Accession: I56191

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:D13556; NID:g436580; PIDN:BAA02754.1; PID:g436581

C;Keywords: T-cell receptor

Query Match 10.3%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 13 RKK 15

RESULT 37

GCCB

glucagon - Chinchilla brevicaudata

C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998

C;Accession: A60413

R;Eng, J.; Kleinman, W.A.; Chu, L.S.

Peptides 11, 683-685, 1990

A;Title: Purification of peptide hormones from chinchilla pancreas by chemical assay.

A;Reference number: A60413; MUID:91045327; PMID:2235678

A;Accession: A60413

A;Molecule type: protein

A;Residues: 1-29 <ENG>

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15
|||
Db 12 KHL 14

RESULT 38

S39968

probable hydro-lyase (EC 4.2.1.-) [similarity] - Streptomyces griseus (fragment)

N;Alternate names: hypothetical protein 6

C;Species: Streptomyces griseus

C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 18-Aug-2000

C;Accession: S39968

R;Kruegel, H.; Schumann, G.; Haenel, F.; Fiedler, G.

Mol. Gen. Genet. 241, 193-202, 1993

A;Title: Nucleotide sequence analysis of five putative Streptomyces griseus genes, one of which complements an early function in daunorubicin biosynthesis that is linked to a putative gene cluster involved in TDP-daunosamine formation.

A;Reference number: S39963; MUID:94049680; PMID:8232204

A;Accession: S39968

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-29 <KRU>

A;Cross-references: EMBL:X73148; NID:g407882; PIDN:CAA51673.1; PID:e80351;
PID:g1235599

C;Superfamily: erythromycin resistance protein

C;Keywords: antibiotic resistance; carbon-oxygen lyase; hydro-lyase

Query Match 10.3%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ERV 21
|||
Db 16 ERV 18

RESULT 39

A61509

islet amyloid polypeptide - cougar (fragment)

C;Species: Felis concolor (cougar)

C;Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 11-May-2000

C;Accession: A61509

R;Johnson, K.H.; Wernstedt, C.; O'Brien, T.D.; Westermark, P.

Comp. Biochem. Physiol. B 98, 115-119, 1991

A;Title: Amyloid in the pancreatic islets of the cougar (Felis concolor) is derived from islet amyloid polypeptide (IAPP).

A;Reference number: A61509; MUID:91284578; PMID:2060275

A;Accession: A61509

A;Molecule type: protein

A;Residues: 1-29 <JOH>

C;Superfamily: calcitonin

Query Match 10.3%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 22 NLG 24

RESULT 40

S17147

galanin - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996

C;Accession: S17147

R;Norberg, A.; Sillard, R.; Carlquist, M.; Joernvall, H.; Mutt, V.

FEBS Lett. 288, 151-153, 1991

A;Title: Chemical detection of natural peptides by specific structures.

Isolation of chicken galanin by monitoring for its N-terminal dipeptide, and determination of the amino acid sequence.

A;Reference number: S17147; MUID:91348254; PMID:1715289

A;Accession: S17147

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-29 <NOR>

C;Superfamily: galanin

Query Match 10.3%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
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Db 4 LNS 6

Search completed: January 14, 2004, 10:37:28
Job time : 9.58255 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 19.514 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-167
Perfect score: 29
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	29	100.0	30	11	US-09-843-221A-166	Sequence 166, App
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6	29	100.0	31	11	US-09-843-221A-27	Sequence 27, Appl
7	29	100.0	31	11	US-09-843-221A-165	Sequence 165, App
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9	29	100.0	34	9	US-09-169-786-3	Sequence 3, Appli
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261	4	13.8	35	12	US-10-012-952A-147	Sequence 147, App
262	4	13.8	35	12	US-10-062-599-138	Sequence 138, App
263	4	13.8	35	15	US-10-133-128-75	Sequence 75, Appl
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275	4	13.8	37	8	US-08-851-965-25	Sequence 25, Appl
276	4	13.8	37	8	US-08-851-965-26	Sequence 26, Appl
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808	3	10.3	28	15	US-10-187-051-147	Sequence 147, App
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815	3	10.3	28	15	US-10-023-282-638	Sequence 638, App
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954	3	10.3	29	12	US-09-963-693-71	Sequence 71, Appl
955	3	10.3	29	12	US-10-105-232-319	Sequence 319, App
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957	3	10.3	29	12	US-10-280-066-334	Sequence 334, App
958	3	10.3	29	12	US-10-289-135A-25	Sequence 25, Appl
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968	3	10.3	29	12	US-10-189-437-499	Sequence 499, App

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974	3	10.3	29	12	US-09-818-683-512	Sequence 512, App
975	3	10.3	29	12	US-09-818-683-529	Sequence 529, App
976	3	10.3	29	12	US-09-818-683-581	Sequence 581, App
977	3	10.3	29	12	US-10-350-719-123	Sequence 123, Appl
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979	3	10.3	29	12	US-10-074-024-284	Sequence 284, App
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981	3	10.3	29	12	US-10-154-884B-11109	Sequence 11109, A
982	3	10.3	29	12	US-10-227-577-638	Sequence 638, App
983	3	10.3	29	12	US-10-227-577-674	Sequence 674, App
984	3	10.3	29	12	US-10-264-049-3305	Sequence 3305, Ap
985	3	10.3	29	12	US-10-387-977-16	Sequence 16, Appl
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991	3	10.3	29	15	US-10-214-188-13	Sequence 13, Appl
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993	3	10.3	29	15	US-10-014-162-47	Sequence 47, Appl
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995	3	10.3	29	15	US-10-018-103A-4	Sequence 4, Appli
996	3	10.3	29	15	US-10-018-103A-7	Sequence 7, Appli
997	3	10.3	29	15	US-10-045-465-12	Sequence 12, Appl
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999	3	10.3	29	15	US-10-097-065-380	Sequence 380, App
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ALIGNMENTS

RESULT 1

US-09-843-221A-51

; Sequence 51, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 3

US-09-843-221A-39

; Sequence 39, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39

Query Match 100.0%; Score 29; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 4

US-09-843-221A-166

; Sequence 166, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860


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; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-27

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Query Match          100.0%;  Score 29;  DB 11;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 1.1e-22;
Matches 29;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

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RESULT 7

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US-09-843-221A-165
; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165

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RESULT 9

US-09-169-786-3

; Sequence 3, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-169-786-3

Query Match 100.0%; Score 29; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 10

US-09-928-047B-6

; Sequence 6, Application US/09928047B
 ; Patent No. US20020160945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantor, Thomas
 ; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
 ; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
 ; FILE REFERENCE: 53221-20002.00
 ; CURRENT APPLICATION NUMBER: US/09/928,047B
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/224,446
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-047B-6

Query Match 100.0%; Score 29; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 11

US-09-843-221A-16

; Sequence 16, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-843-221A-16

Query Match 100.0%; Score 29; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 12

US-09-843-221A-161

; Sequence 161, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28


```
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-161
```

```
Query Match          100.0%; Score 29; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 13

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US-09-928-048A-6
; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6
```

```
Query Match          100.0%; Score 29; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 14

```
US-10-361-928-8
; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
```

```
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ser
US-10-361-928-8
```

```
Query Match          100.0%;   Score 29;   DB 12;   Length 34;
Best Local Similarity 100.0%;   Pred. No. 1.2e-22;
Matches 29;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
          |||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 15

```
US-10-340-484-15
; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 34
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 100.0%; Score 29; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 16

US-10-340-484-16
; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 100.0%; Score 29; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 17

US-10-016-403-5
; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

```

```

Query Match          100.0%;  Score 29;  DB 14;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.2e-22;
Matches 29;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 18

US-10-097-079-1

; Sequence 1, Application US/10097079

; Publication No. US20020132973A1

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.

; Morize, Isabelle

; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, Mailstop 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/097,079
 ; FILING DATE: 13-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/228,990
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 60/046,472
 ; FILING DATE: 14-MAY-1997
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Martin Esq., Michael B.
 ; REGISTRATION NUMBER: 37,521
 ; REFERENCE/DOCKET NUMBER: A2678B-WO
 ;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-2793
 ; TELEFAX: (610) 454-3808
 ;
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: No. US20020132973A1 Relevant
 ;
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 ;
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-097-079-1

Query Match 100.0%; Score 29; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 19
 US-10-168-185-9
 ; Sequence 9, Application US/10168185
 ; Publication No. US20030175802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Armbruster, Franz Paul
 ; APPLICANT: Missbichler, Albert
 ; APPLICANT: Schmidt-Gayk, Heinrich
 ; APPLICANT: Roth, Heinz-Jurgen

; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-9

Query Match 100.0%; Score 29; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 20

US-09-169-786-4
; Sequence 4, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-4

Query Match 100.0%; Score 29; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 21

US-09-843-221A-14

```
; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-14
```

```
Query Match          100.0%; Score 29; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 22

```
US-10-245-707-1
; Sequence 1, Application US/10245707
; Publication No. US20030171282A1
; GENERAL INFORMATION:
; APPLICANT: Patton, John S.
; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments of Parathyroid
Hormone
; FILE REFERENCE: 032055-047
; CURRENT APPLICATION NUMBER: US/10/245,707
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/577,264
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/128,401
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/625,586
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: US 08/232,849
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 07/953,397
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 1
```



```
; Sequence 168, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-168
```

```
Query Match          96.6%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        ||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
```

RESULT 25

```
US-09-843-221A-43
; Sequence 43, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
```

; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-43

Query Match 96.6%; Score 28; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 26

US-10-361-928-3
; Sequence 3, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-3

Query Match 96.6%; Score 28; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Db ||||| 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 27

US-10-361-928-6

; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 96.6%; Score 28; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
 |||||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 28

US-09-843-221A-20

; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-20

Query Match 96.6%; Score 28; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 29

US-10-361-928-1

; Sequence 1, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-10-361-928-1

Query Match 96.6%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 30

US-10-361-928-2
; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-2

Query Match 96.6%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 31

US-10-361-928-5
; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800

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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-10-361-928-5

```

```

Query Match          96.6%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
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Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

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RESULT 32

US-10-016-403-7

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; Sequence 7, Application US/10016403
; Publication No. US20020107505A1
;   GENERAL INFORMATION:
;   APPLICANT: Holladay, Leslie A.
;   TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
;                       INCREASE ELECTROTRANSPORT FLUX
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
;       STREET: 25 West Main Street
;       CITY: Madison
;       STATE: WI
;       COUNTRY: USA
;       ZIP: 53701-2236
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/016,403
;       FILING DATE: 10-Dec-2001
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/466,610
;       FILING DATE: 1995-JUN-06
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Frenchick, Grady J.
;       REGISTRATION NUMBER: 29,018
;       REFERENCE/DOCKET NUMBER: 8734.28
;   TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-016-403-7

```

```

Query Match          96.6%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        ||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

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RESULT 33

```

US-09-843-221A-15
; Sequence 15, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-15

```

```

Query Match          96.6%; Score 28; DB 11; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

Db |||||
1 VSEIQLMHNLGKHLNSMERVEWLRKKLQ 28

RESULT 34

US-09-843-221A-50
; Sequence 50, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-50

Query Match 89.7%; Score 26; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
 |||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 35

US-09-843-221A-28
; Sequence 28, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-28

Query Match 89.7%; Score 26; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 36

US-10-031-874A-206

; Sequence 206, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID
; APPLICANT: DUBUC, GINETTE
; APPLICANT: NARANG, SARAN
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
; FILE REFERENCE: 11054-1
; CURRENT APPLICATION NUMBER: US/10/031,874A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/207,234
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 206
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Lama glama
US-10-031-874A-206

Query Match 89.7%; Score 26; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 37

US-10-372-095-24

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; Sequence 24, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-095-24
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Query Match          89.7%; Score 26; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 EIQLMHNLGKHLNSMERVEWLRKKLQ 29
        |||||||||||||||||||||||||
Db      4 EIQLMHNLGKHLNSMERVEWLRKKLQ 29
```

RESULT 38

US-09-843-221A-32

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; Sequence 32, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 79.3%; Score 23; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKLQ 29
|||||
Db 1 LMHNLGKHLNSMERVEWLRKKLQ 23

RESULT 39

US-10-016-403-6

; Sequence 6, Application US/10016403
; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 21.6822 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-167
Perfect score: 29
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	14	48.3	31	11	Q91Y90	Q91y90 peromyscus
2	14	48.3	31	11	Q91Y91	Q91y91 peromyscus
3	5	17.2	34	5	O17148	O17148 echinococcu
4	5	17.2	34	16	Q97K50	Q97k50 clostridium
5	5	17.2	34	17	Q9HR65	Q9hr65 halobacteri
6	5	17.2	35	11	Q8BTB9	Q8btb9 mus musculu
7	4	13.8	28	10	O24285	O24285 pinus radia
8	4	13.8	28	10	Q8GZQ8	Q8gzb8 hordeum vul
9	4	13.8	29	2	Q49148	Q49148 methylobact
10	4	13.8	29	4	Q9UCL2	Q9ucl2 homo sapien
11	4	13.8	29	4	Q96PP3	Q96pp3 homo sapien
12	4	13.8	29	5	Q25603	Q25603 onchocerca
13	4	13.8	29	13	O13043	O13043 scyliorhinu
14	4	13.8	30	2	Q9JMV3	Q9jmv3 escherichia
15	4	13.8	30	4	Q9UBV5	Q9ubv5 homo sapien
16	4	13.8	30	16	Q8DZP7	Q8dzb7 streptococc
17	4	13.8	31	1	Q55314	Q55314 sulfolobus
18	4	13.8	31	4	Q8NEI8	Q8nei8 homo sapien
19	4	13.8	31	8	Q9MS77	Q9ms77 phacus acum
20	4	13.8	31	16	O50669	O50669 borrelia bu
21	4	13.8	32	11	Q9QZQ2	Q9qzb2 mus musculu
22	4	13.8	33	5	Q95SD4	Q95sd4 drosophila
23	4	13.8	33	16	Q9PKX3	Q9pkx3 chlamydia m
24	4	13.8	34	2	Q9ZG81	Q9zg81 chlamydia t
25	4	13.8	34	2	Q8GFK2	Q8gfk2 staphylococ
26	4	13.8	34	13	Q90ZJ4	Q90zb4 gallus gall
27	4	13.8	34	16	Q8G2Q2	Q8g2q2 brucella su
28	4	13.8	35	12	Q8V6J8	Q8v6j8 halovirus h
29	4	13.8	35	16	Q9KQG4	Q9kqg4 vibrio chol
30	4	13.8	35	16	Q97RG6	Q97rg6 streptococc
31	4	13.8	35	16	Q8F102	Q8f102 leptospira
32	4	13.8	36	2	Q53920	Q53920 streptomyce
33	4	13.8	36	2	O68941	O68941 rhodospiril
34	4	13.8	36	4	Q8WXW8	Q8wxw8 homo sapien
35	4	13.8	36	10	Q9SJ63	Q9sj63 arabidopsis
36	4	13.8	36	12	Q9PXD1	Q9pxd1 hepatitis c
37	4	13.8	36	12	Q91D77	Q91d77 ttv-like mi
38	4	13.8	36	13	Q9YHT9	Q9yht9 brachydanio
39	4	13.8	36	16	Q97S91	Q97s91 streptococc
40	4	13.8	37	2	Q8KYJ0	Q8kyj0 bacillus an
41	4	13.8	37	5	Q9N2L2	Q9n2l2 caenorhabdi
42	4	13.8	37	10	Q39942	Q39942 helianthus
43	4	13.8	37	13	Q8AWW8	Q8aww8 oncorhynchu
44	4	13.8	37	16	Q8F6U2	Q8f6u2 leptospira
45	4	13.8	37	16	Q8F5H3	Q8f5h3 leptospira
46	4	13.8	37	16	Q8F419	Q8f419 leptospira
47	4	13.8	37	16	Q8EXV9	Q8exv9 leptospira
48	4	13.8	38	2	Q8KWH7	Q8kwh7 lactobacill
49	4	13.8	38	5	Q9NBE3	Q9nbe3 chironomus
50	4	13.8	38	5	Q9NBE5	Q9nbe5 chironomus
51	4	13.8	38	5	Q9NBE8	Q9nbe8 chironomus
52	4	13.8	38	5	Q9NBE4	Q9nbe4 chironomus
53	4	13.8	38	5	Q9NBE7	Q9nbe7 chironomus
54	4	13.8	38	11	Q91VC8	Q91vc8 mus musculu
55	4	13.8	38	13	Q8AWW9	Q8aww9 oncorhynchu
56	4	13.8	38	16	Q8E0D2	Q8e0d2 streptococc
57	4	13.8	39	2	Q8GPQ8	Q8gpb8 pseudomonas

58	4	13.8	39	10	Q9FEY1	Q9fey1 heterocapsa
59	4	13.8	39	12	Q68847	Q68847 hepatitis c
60	4	13.8	39	12	Q68845	Q68845 hepatitis c
61	4	13.8	39	12	Q68846	Q68846 hepatitis c
62	4	13.8	39	13	Q90776	Q90776 gallus gall
63	4	13.8	39	16	Q9KYH4	Q9kyh4 streptomyce
64	4	13.8	39	16	Q8F0C7	Q8f0c7 leptospira
65	4	13.8	39	16	Q8EZ33	Q8ez33 leptospira
66	4	13.8	40	2	Q8GCS7	Q8gcs7 eubacterium
67	4	13.8	40	4	P78340	P78340 homo sapien
68	4	13.8	40	6	Q29283	Q29283 sus scrofa
69	4	13.8	40	10	Q8H192	Q8h192 arabidopsis
70	4	13.8	40	12	Q91JZ7	Q91jz7 hepatitis c
71	4	13.8	40	12	Q8V647	Q8v647 rabies viru
72	3	10.3	28	2	Q01303	Q01303 treponema p
73	3	10.3	28	2	Q05574	Q05574 prochloroth
74	3	10.3	28	2	Q9ZB83	Q9zb83 vibrio angu
75	3	10.3	28	3	Q8TGT8	Q8tgt8 saccharomyc
76	3	10.3	28	4	Q96SD9	Q96sd9 homo sapien
77	3	10.3	28	4	Q16326	Q16326 homo sapien
78	3	10.3	28	4	Q96EU0	Q96eu0 homo sapien
79	3	10.3	28	4	O75980	O75980 homo sapien
80	3	10.3	28	4	O95737	O95737 homo sapien
81	3	10.3	28	5	Q8MUW0	Q8muw0 schistosoma
82	3	10.3	28	5	Q8MPY2	Q8mpy2 caenorhabdi
83	3	10.3	28	5	Q9BM68	Q9bm68 glottidia p
84	3	10.3	28	5	Q9BJE4	Q9bje4 pauropus sp
85	3	10.3	28	6	O62821	O62821 bubalus bub
86	3	10.3	28	8	Q8WBC8	Q8wbc8 cucurbita e
87	3	10.3	28	8	Q9TIE9	Q9tie9 centella er
88	3	10.3	28	8	Q9TIE8	Q9tie8 centella as
89	3	10.3	28	8	Q9MR96	Q9mr96 crocodylus
90	3	10.3	28	8	Q9TIE6	Q9tie6 centella hi
91	3	10.3	28	8	Q9ZYS4	Q9zys4 leishmania
92	3	10.3	28	8	Q9MR94	Q9mr94 chelonia my
93	3	10.3	28	8	Q9TIE7	Q9tie7 centella tr
94	3	10.3	28	8	Q8HS23	Q8hs23 pisum sativ
95	3	10.3	28	8	Q8HS11	Q8hs11 spathiphyll
96	3	10.3	28	8	Q8HS07	Q8hs07 welwitschia
97	3	10.3	28	8	Q8HKF0	Q8hkf0 rhipicephal
98	3	10.3	28	9	Q9AZJ9	Q9azj9 bacterioph
99	3	10.3	28	10	Q8S526	Q8s526 ipomoea bat
100	3	10.3	28	10	Q8W232	Q8w232 zea mays (m
101	3	10.3	28	10	Q944P1	Q944p1 manihot esc
102	3	10.3	28	11	Q9ESI4	Q9esi4 petromus ty
103	3	10.3	28	11	Q9ESI5	Q9esi5 thryonomys
104	3	10.3	28	11	Q9ESI6	Q9esi6 hystrix afr
105	3	10.3	28	11	Q99PL9	Q99pl9 mus musculu
106	3	10.3	28	11	Q9ESI2	Q9esi2 cryptomys h
107	3	10.3	28	11	Q9EP60	Q9ep60 heliophobi
108	3	10.3	28	11	Q9ESI0	Q9esi0 cryptomys s
109	3	10.3	28	11	Q91XP0	Q91xp0 rattus norv
110	3	10.3	28	11	P70651	P70651 mus sp. bet
111	3	10.3	28	11	Q9EP59	Q9ep59 georychus c
112	3	10.3	28	11	Q9ESI1	Q9esi1 cryptomys d
113	3	10.3	28	11	P97914	P97914 rattus norv
114	3	10.3	28	11	Q9EP61	Q9ep61 heteroceph

115	3	10.3	28	11	Q9ESH8	Q9esh8 bathyergus
116	3	10.3	28	11	Q9ESH9	Q9esh9 bathyergus
117	3	10.3	28	11	Q9QXB4	Q9qxb4 mus musculu
118	3	10.3	28	11	Q9ESI3	Q9esi3 cryptomys h
119	3	10.3	28	12	Q67786	Q67786 human adeno
120	3	10.3	28	12	Q83181	Q83181 cauliflower
121	3	10.3	28	12	Q68552	Q68552 hepatitis c
122	3	10.3	28	12	Q9WNI4	Q9wni4 tt virus. o
123	3	10.3	28	13	Q9PRE8	Q9pre8 oryzias lat
124	3	10.3	28	13	Q9PRI9	Q9pri9 amia calva
125	3	10.3	28	13	Q9PRN8	Q9prn8 carassius a
126	3	10.3	28	15	O71346	O71346 human endog
127	3	10.3	28	15	Q9QEY3	Q9qey3 human immun
128	3	10.3	28	16	Q8NVB8	Q8nvb8 staphylococ
129	3	10.3	28	16	Q8ENT7	Q8ent7 oceanobacil
130	3	10.3	28	16	Q8CK95	Q8ck95 yersinia pe
131	3	10.3	29	2	Q9ZGG4	Q9zgg4 heliobacill
132	3	10.3	29	2	Q54200	Q54200 streptomyce
133	3	10.3	29	2	Q9X3E3	Q9x3e3 prochloroco
134	3	10.3	29	2	Q9X3J9	Q9x3j9 prochloroco
135	3	10.3	29	2	Q47650	Q47650 escherichia
136	3	10.3	29	2	Q9AKV1	Q9akv1 neisseria g
137	3	10.3	29	2	Q9R526	Q9r526 vibrio chol
138	3	10.3	29	3	P78747	P78747 saccharomyc
139	3	10.3	29	4	Q9Y3G1	Q9y3g1 homo sapien
140	3	10.3	29	4	Q9UN87	Q9un87 homo sapien
141	3	10.3	29	4	Q9H465	Q9h465 homo sapien
142	3	10.3	29	4	Q8NEF6	Q8nef6 homo sapien
143	3	10.3	29	4	Q8TDW8	Q8tdw8 homo sapien
144	3	10.3	29	4	Q96IR5	Q96ir5 homo sapien
145	3	10.3	29	4	Q9BSQ3	Q9bsq3 homo sapien
146	3	10.3	29	5	Q95VB2	Q95vb2 spirometra
147	3	10.3	29	5	Q95NF4	Q95nf4 drosophila
148	3	10.3	29	5	Q8T936	Q8t936 folsomia ca
149	3	10.3	29	6	Q9TRG5	Q9trg5 sus scrofa
150	3	10.3	29	8	Q8WBB9	Q8wbb9 cucurbita f
151	3	10.3	29	8	Q8W7W7	Q8w7w7 cucurbita p
152	3	10.3	29	8	Q9GF70	Q9gf70 trochodendr
153	3	10.3	29	8	Q8W7W4	Q8w7w4 cucurbita a
154	3	10.3	29	8	Q8W7W6	Q8w7w6 cucurbita p
155	3	10.3	29	8	Q8WBC1	Q8wbc1 cucurbita o
156	3	10.3	29	8	Q9B5Z6	Q9b5z6 pseudostylo
157	3	10.3	29	8	Q8W7W5	Q8w7w5 cucurbita p
158	3	10.3	29	8	Q9G370	Q9g370 draco blanf
159	3	10.3	29	8	Q8WBD0	Q8wbd0 cucurbita a
160	3	10.3	29	8	Q8WBB6	Q8wbb6 citrullus l
161	3	10.3	29	8	Q8W7W9	Q8w7w9 cucurbita f
162	3	10.3	29	8	Q8W7W8	Q8w7w8 cucurbita m
163	3	10.3	29	8	Q8HS21	Q8hs21 rheum x cul
164	3	10.3	29	9	Q9FZX6	Q9fzx6 bacterioph
165	3	10.3	29	10	P82196	P82196 spinacia ol
166	3	10.3	29	11	Q9Z2C0	Q9z2c0 mus musculu
167	3	10.3	29	11	Q921Z6	Q921z6 mus musculu
168	3	10.3	29	11	Q9Z2C1	Q9z2c1 mus musculu
169	3	10.3	29	11	O70564	O70564 mus musculu
170	3	10.3	29	11	Q9QY65	Q9qy65 mus musculu
171	3	10.3	29	11	Q62300	Q62300 mus musculu

172	3	10.3	29	11	O08980	O08980	mus musculu
173	3	10.3	29	11	Q8CGM8	Q8cgm8	mus musculu
174	3	10.3	29	12	Q91HB1	Q91hbl	porcine cir
175	3	10.3	29	12	O92646	O92646	hepatitis e
176	3	10.3	29	12	Q919A5	Q919a5	porcine rep
177	3	10.3	29	12	Q919A7	Q919a7	porcine rep
178	3	10.3	29	12	Q86872	Q86872	cauliflower
179	3	10.3	29	12	O92648	O92648	hepatitis e
180	3	10.3	29	12	O56835	O56835	vibrio chol
181	3	10.3	29	13	P82235	P82235	rana tempor
182	3	10.3	29	13	Q8AYR0	Q8ayr0	oryzias lat
183	3	10.3	29	13	Q8AWC2	Q8awc2	gallus gall
184	3	10.3	29	15	O72001	O72001	human endog
185	3	10.3	29	15	O71342	O71342	human endog
186	3	10.3	29	15	O71339	O71339	human endog
187	3	10.3	29	15	O71347	O71347	human endog
188	3	10.3	29	15	O71340	O71340	human endog
189	3	10.3	29	15	O71343	O71343	human endog
190	3	10.3	29	15	Q9IQJ8	Q9iqj8	human immun
191	3	10.3	29	15	O71991	O71991	human endog
192	3	10.3	29	15	Q9IQJ1	Q9iqj1	human immun
193	3	10.3	29	15	O71994	O71994	human endog
194	3	10.3	29	15	O71341	O71341	human endog
195	3	10.3	29	15	O71345	O71345	human endog
196	3	10.3	29	15	O71336	O71336	human endog
197	3	10.3	29	15	O71344	O71344	human endog
198	3	10.3	29	15	O71338	O71338	human endog
199	3	10.3	29	15	O71992	O71992	human endog
200	3	10.3	29	15	O71337	O71337	human endog
201	3	10.3	29	15	Q9IQJ9	Q9iqj9	human immun
202	3	10.3	29	15	O71997	O71997	human endog
203	3	10.3	29	15	O71335	O71335	human endog
204	3	10.3	29	16	Q9JZN6	Q9jzn6	neisseria m
205	3	10.3	29	16	Q8X419	Q8x419	escherichia
206	3	10.3	30	2	Q9JP75	Q9jp75	salmonella
207	3	10.3	30	2	Q9L8W9	Q9l8w9	streptomyce
208	3	10.3	30	2	Q9L8X1	Q9l8x1	streptomyce
209	3	10.3	30	2	Q9R4Z6	Q9r4z6	clostridium
210	3	10.3	30	2	Q9REI5	Q9rei5	acidiphiliu
211	3	10.3	30	2	Q9R4J2	Q9r4j2	helicobacte
212	3	10.3	30	2	Q8VUW9	Q8vuw9	staphylococ
213	3	10.3	30	2	Q9R4I5	Q9r4i5	mycoplasma
214	3	10.3	30	2	Q9R5Q3	Q9r5q3	leuconostoc
215	3	10.3	30	2	Q93GF6	Q93gf6	staphylococ
216	3	10.3	30	2	Q45966	Q45966	coxiella bu
217	3	10.3	30	2	Q9R5C4	Q9r5c4	comamonas.
218	3	10.3	30	2	Q9R5K3	Q9r5k3	leptospira
219	3	10.3	30	2	Q9R4I6	Q9r4i6	mycoplasma
220	3	10.3	30	2	Q9RER6	Q9rer6	enterobacte
221	3	10.3	30	3	Q8TGM3	Q8tgm3	saccharomyc
222	3	10.3	30	3	Q9URB0	Q9urb0	candida alb
223	3	10.3	30	4	Q16330	Q16330	homo sapien
224	3	10.3	30	4	O95595	O95595	homo sapien
225	3	10.3	30	4	P78460	P78460	homo sapien
226	3	10.3	30	4	Q8N563	Q8n563	homo sapien
227	3	10.3	30	4	P78542	P78542	homo sapien
228	3	10.3	30	4	Q8IU66	Q8iu66	homo sapien

229	3	10.3	30	5	Q8SZJ6	Q8szj6 drosophila
230	3	10.3	30	5	Q9TWH7	Q9twh7 ancylostoma
231	3	10.3	30	5	P82214	P82214 bombyx mori
232	3	10.3	30	6	Q9BDK1	Q9bdk1 bos taurus
233	3	10.3	30	6	Q9TTF9	Q9ttf9 ateles belz
234	3	10.3	30	8	Q8W7L1	Q8w7l1 cucurbita m
235	3	10.3	30	8	Q8W7K9	Q8w7k9 cucurbita p
236	3	10.3	30	8	Q8W7H8	Q8w7h8 cucurbita a
237	3	10.3	30	8	Q8WBC2	Q8wbc2 cucurbita o
238	3	10.3	30	8	Q8W7K8	Q8w7k8 cucurbita p
239	3	10.3	30	8	Q8W7H6	Q8w7h6 cucurbita m
240	3	10.3	30	8	Q8WBC4	Q8wbc4 cucurbita p
241	3	10.3	30	8	Q8W7L2	Q8w7l2 cucurbita a
242	3	10.3	30	8	Q8WBC6	Q8wbc6 cucurbita a
243	3	10.3	30	8	Q8WBB7	Q8wbb7 sechium edu
244	3	10.3	30	8	Q99328	Q99328 meloidogyne
245	3	10.3	30	8	Q8W7H7	Q8w7h7 cucurbita e
246	3	10.3	30	8	Q8WBC0	Q8wbc0 cucurbita f
247	3	10.3	30	8	Q9T2T8	Q9t2t8 bos taurus
248	3	10.3	30	8	Q8W7L0	Q8w7l0 cucurbita p
249	3	10.3	30	8	Q8HKG1	Q8hkg1 rhipicephal
250	3	10.3	30	9	Q8W674	Q8w674 enterobacte
251	3	10.3	30	10	O23933	O23933 flaveria tr
252	3	10.3	30	10	Q8RUD1	Q8rud1 zea mays (m
253	3	10.3	30	10	Q93WY2	Q93wy2 oryza sativ
254	3	10.3	30	11	Q63885	Q63885 mus sp. cys
255	3	10.3	30	11	O88549	O88549 mesocricetu
256	3	10.3	30	11	Q8VDL1	Q8vdl1 mus musculu
257	3	10.3	30	11	Q9QV18	Q9qv18 rattus sp.
258	3	10.3	30	11	Q9QV14	Q9qv14 mus sp. col
259	3	10.3	30	11	Q9QV19	Q9qv19 rattus sp.
260	3	10.3	30	11	Q10753	Q10753 rattus norv
261	3	10.3	30	11	Q8BR32	Q8br32 mus musculu
262	3	10.3	30	12	Q91HB7	Q91hb7 tt virus. o
263	3	10.3	30	12	Q91HC4	Q91hc4 tt virus. o
264	3	10.3	30	12	Q9IJV5	Q9ijv5 norwalk vir
265	3	10.3	30	12	Q86870	Q86870 cauliflower
266	3	10.3	30	12	Q91HC3	Q91hc3 tt virus. o
267	3	10.3	30	12	Q9WLK3	Q9wlk3 hepatitis e
268	3	10.3	30	12	Q91HC0	Q91hc0 tt virus. o
269	3	10.3	30	13	O42551	O42551 brachydanio
270	3	10.3	30	13	Q9PRW0	Q9prw0 struthio ca
271	3	10.3	30	13	Q9PT00	Q9pt00 oncorhynch
272	3	10.3	30	15	Q86599	Q86599 human endog
273	3	10.3	30	15	Q991P5	Q991p5 human immun
274	3	10.3	30	16	O50822	O50822 borrelia bu
275	3	10.3	30	16	Q9X0W9	Q9x0w9 thermotoga
276	3	10.3	30	16	Q9PP53	Q9pp53 campylobact
277	3	10.3	30	16	Q9KU55	Q9ku55 vibrio chol
278	3	10.3	30	16	Q9JWF4	Q9jwf4 neisseria m
279	3	10.3	30	16	Q97SX5	Q97sx5 streptococc
280	3	10.3	30	16	Q9K1W7	Q9k1w7 chlamydia p
281	3	10.3	30	16	Q8U566	Q8u566 agrobacteri
282	3	10.3	30	16	Q8KE55	Q8ke55 chlorobium
283	3	10.3	30	16	Q93RS7	Q93rs7 streptomyce
284	3	10.3	30	16	Q8G1R1	Q8glr1 brucella su
285	3	10.3	30	16	Q8FZX9	Q8fzx9 brucella su

286	3	10.3	30	16	Q8CU88	Q8cu88	staphylococ
287	3	10.3	30	17	Q8ZZF0	Q8zzf0	pyrobaculum
288	3	10.3	30	17	Q8ZVL0	Q8zvl0	pyrobaculum
289	3	10.3	31	2	Q9S619	Q9s619	prochloroco
290	3	10.3	31	2	Q8KYK0	Q8kyk0	bacillus an
291	3	10.3	31	2	Q9JMV2	Q9jmv2	escherichia
292	3	10.3	31	2	Q9X3C3	Q9x3c3	prochloroco
293	3	10.3	31	2	O68825	O68825	pseudomonas
294	3	10.3	31	2	Q93GF7	Q93gf7	staphylococ
295	3	10.3	31	2	Q47323	Q47323	escherichia
296	3	10.3	31	2	Q9RHF9	Q9rhf9	acinetobact
297	3	10.3	31	2	Q9R4X1	Q9r4x1	treponema d
298	3	10.3	31	2	Q8KYI9	Q8kyi9	bacillus an
299	3	10.3	31	2	Q8RTS5	Q8rts5	uncultured
300	3	10.3	31	2	Q8L3D3	Q8l3d3	colwellia m
301	3	10.3	31	3	O94120	O94120	saccharomyc
302	3	10.3	31	4	Q96A45	Q96a45	homo sapien
303	3	10.3	31	4	Q9UHM9	Q9uhm9	homo sapien
304	3	10.3	31	4	Q9UEA9	Q9uea9	homo sapien
305	3	10.3	31	4	Q8N5X3	Q8n5x3	homo sapien
306	3	10.3	31	4	Q9BXM4	Q9bxm4	homo sapien
307	3	10.3	31	4	Q9UDE5	Q9ude5	homo sapien
308	3	10.3	31	5	Q8IQV3	Q8iqv3	drosophila
309	3	10.3	31	5	Q8IEY3	Q8iey3	trypanosoma
310	3	10.3	31	6	Q8MI94	Q8mi94	tupaia tana
311	3	10.3	31	6	Q9GLD6	Q9gld6	sus scrofa
312	3	10.3	31	6	Q8MIH5	Q8mih5	canis famil
313	3	10.3	31	6	O77625	O77625	bos taurus
314	3	10.3	31	6	Q8MIC3	Q8mic3	ochotona pr
315	3	10.3	31	6	Q95LC0	Q95lc0	sus scrofa
316	3	10.3	31	6	Q9N1C8	Q9nlc8	ovis aries
317	3	10.3	31	6	Q8MIC9	Q8mic9	nycticebus
318	3	10.3	31	6	Q9GKL4	Q9gkl4	canis famil
319	3	10.3	31	6	Q8MIG4	Q8mig4	cynocephalu
320	3	10.3	31	6	Q9XSB9	Q9xsb9	ateles belz
321	3	10.3	31	7	Q29868	Q29868	homo sapien
322	3	10.3	31	8	Q9MNM2	Q9mnm2	bufo americ
323	3	10.3	31	8	Q9MS59	Q9ms59	euglena san
324	3	10.3	31	8	O80011	O80011	enallagma a
325	3	10.3	31	8	Q9MS62	Q9ms62	euglena myx
326	3	10.3	31	8	Q34922	Q34922	limulus pol
327	3	10.3	31	8	Q8WEJ4	Q8wej4	gnetum gnem
328	3	10.3	31	8	Q9MS74	Q9ms74	euglena ana
329	3	10.3	31	8	Q9MS68	Q9ms68	euglena des
330	3	10.3	31	8	Q8M9Y3	Q8m9y3	chaetosphae
331	3	10.3	31	8	Q9MS53	Q9ms53	euglena vir
332	3	10.3	31	8	Q9MNL2	Q9mnl2	torrentophr
333	3	10.3	31	8	Q9MS56	Q9ms56	euglena ste
334	3	10.3	31	8	Q9MS78	Q9ms78	phacus acum
335	3	10.3	31	8	Q9MNL3	Q9mnl3	torrentophr
336	3	10.3	31	9	Q38499	Q38499	bacteriopha
337	3	10.3	31	10	Q9XIT0	Q9xit0	glycine max
338	3	10.3	31	10	Q8LKB4	Q8lkb4	musa acumin
339	3	10.3	31	11	Q8K1W2	Q8k1w2	cavia porce
340	3	10.3	31	11	Q9QXB6	Q9qxb6	mus musculu
341	3	10.3	31	11	Q99KK6	Q99kk6	mus musculu
342	3	10.3	31	11	Q8K1P4	Q8k1p4	sciurus vul

343	3	10.3	31	11	Q8CGM7	Q8cgm7	mus	musculu
344	3	10.3	31	12	Q919E5	Q919e5	human	papil
345	3	10.3	31	12	Q919E4	Q919e4	human	papil
346	3	10.3	31	12	O56713	O56713	hepatitis	c
347	3	10.3	31	12	Q919F7	Q919f7	human	papil
348	3	10.3	31	12	Q919E6	Q919e6	human	papil
349	3	10.3	31	12	O56692	O56692	hepatitis	c
350	3	10.3	31	12	Q919F3	Q919f3	human	papil
351	3	10.3	31	12	O56707	O56707	hepatitis	c
352	3	10.3	31	12	O56687	O56687	hepatitis	c
353	3	10.3	31	12	Q919F8	Q919f8	human	papil
354	3	10.3	31	12	O56691	O56691	hepatitis	c
355	3	10.3	31	12	Q919E1	Q919e1	human	papil
356	3	10.3	31	12	O56701	O56701	hepatitis	c
357	3	10.3	31	12	O56694	O56694	hepatitis	c
358	3	10.3	31	12	Q919D9	Q919d9	human	papil
359	3	10.3	31	12	Q919F6	Q919f6	human	papil
360	3	10.3	31	12	Q919E3	Q919e3	human	papil
361	3	10.3	31	12	O56712	O56712	hepatitis	c
362	3	10.3	31	12	Q919E8	Q919e8	human	papil
363	3	10.3	31	12	O56710	O56710	hepatitis	c
364	3	10.3	31	12	O56688	O56688	hepatitis	c
365	3	10.3	31	12	O56696	O56696	hepatitis	c
366	3	10.3	31	12	O56695	O56695	hepatitis	c
367	3	10.3	31	12	O56698	O56698	hepatitis	c
368	3	10.3	31	12	O56702	O56702	hepatitis	c
369	3	10.3	31	12	O56703	O56703	hepatitis	c
370	3	10.3	31	12	O56697	O56697	hepatitis	c
371	3	10.3	31	12	Q919F0	Q919f0	human	papil
372	3	10.3	31	12	O56709	O56709	hepatitis	c
373	3	10.3	31	12	Q919F4	Q919f4	human	papil
374	3	10.3	31	12	O56689	O56689	hepatitis	c
375	3	10.3	31	12	Q919F2	Q919f2	human	papil
376	3	10.3	31	12	Q919F1	Q919f1	human	papil
377	3	10.3	31	12	O56711	O56711	hepatitis	c
378	3	10.3	31	12	Q919E2	Q919e2	human	papil
379	3	10.3	31	12	Q919D8	Q919d8	human	papil
380	3	10.3	31	12	O56686	O56686	hepatitis	c
381	3	10.3	31	12	Q9WMX5	Q9wmx5	human	echov
382	3	10.3	31	12	O56690	O56690	hepatitis	c
383	3	10.3	31	12	Q919E9	Q919e9	human	papil
384	3	10.3	31	12	O56706	O56706	hepatitis	c
385	3	10.3	31	12	O56700	O56700	hepatitis	c
386	3	10.3	31	12	O56704	O56704	hepatitis	c
387	3	10.3	31	12	Q919D7	Q919d7	human	papil
388	3	10.3	31	12	Q919F5	Q919f5	human	papil
389	3	10.3	31	12	O56693	O56693	hepatitis	c
390	3	10.3	31	12	O56685	O56685	hepatitis	c
391	3	10.3	31	12	O56708	O56708	hepatitis	c
392	3	10.3	31	12	Q919E0	Q919e0	human	papil
393	3	10.3	31	12	O56705	O56705	hepatitis	c
394	3	10.3	31	12	Q919E7	Q919e7	human	papil
395	3	10.3	31	12	Q914M9	Q914m9	sulfolobus	
396	3	10.3	31	12	O56699	O56699	hepatitis	c
397	3	10.3	31	13	O42540	O42540	brachydanio	
398	3	10.3	31	13	Q91763	Q91763	xenopus	lae
399	3	10.3	31	13	Q9PSU1	Q9psu1	xenopus	lae

400	3	10.3	31	13	Q91816	Q91816 xenopus lae
401	3	10.3	31	15	Q83937	Q83937 ovine lenti
402	3	10.3	31	16	O25108	O25108 helicobacte
403	3	10.3	31	16	O50709	O50709 borrelia bu
404	3	10.3	31	16	O50858	O50858 borrelia bu
405	3	10.3	31	16	O51007	O51007 borrelia bu
406	3	10.3	31	16	Q9PGF2	Q9pgf2 xylella fas
407	3	10.3	31	16	Q9PAW4	Q9paw4 xylella fas
408	3	10.3	31	16	Q97SZ9	Q97sz9 streptococc
409	3	10.3	31	16	Q97SW8	Q97sw8 streptococc
410	3	10.3	31	16	Q97QJ4	Q97qj4 streptococc
411	3	10.3	31	16	Q97QB7	Q97qb7 streptococc
412	3	10.3	31	16	Q97CV6	Q97cv6 streptococc
413	3	10.3	31	16	Q9K2A0	Q9k2a0 chlamydia p
414	3	10.3	31	16	Q9K236	Q9k236 chlamydia p
415	3	10.3	31	16	Q8P9W1	Q8p9w1 xanthomonas
416	3	10.3	31	16	Q8KEV8	Q8kev8 chlorobium
417	3	10.3	31	16	Q8KCQ0	Q8kcq0 chlorobium
418	3	10.3	31	16	Q8KBJ8	Q8kbj8 chlorobium
419	3	10.3	31	16	Q8EIW8	Q8eiw8 shewanella
420	3	10.3	31	16	Q8EI77	Q8ei77 shewanella
421	3	10.3	31	16	Q8E9Y5	Q8e9y5 shewanella
422	3	10.3	31	16	Q8E8G1	Q8e8g1 shewanella
423	3	10.3	31	16	Q8CTA2	Q8cta2 staphylococ
424	3	10.3	32	2	Q9AJ41	Q9aj41 buchnera ap
425	3	10.3	32	2	Q00491	Q00491 streptomyce
426	3	10.3	32	2	Q49249	Q49249 mycoplasma
427	3	10.3	32	2	Q44499	Q44499 anabaena va
428	3	10.3	32	2	Q9S629	Q9s629 prochloroco
429	3	10.3	32	2	Q8KYN3	Q8kyn3 bacillus an
430	3	10.3	32	2	Q44509	Q44509 azotobacter
431	3	10.3	32	2	Q45534	Q45534 bacillus su
432	3	10.3	32	2	Q8VN21	Q8vn21 kluyvera ci
433	3	10.3	32	2	Q9R5Q7	Q9r5q7 aeromonas h
434	3	10.3	32	2	Q8KYM4	Q8kym4 bacillus an
435	3	10.3	32	2	O32493	O32493 bacteroides
436	3	10.3	32	2	Q8VNT6	Q8vnt6 enterobacte
437	3	10.3	32	2	Q9L373	Q9l373 rhizobium l
438	3	10.3	32	2	Q8GF58	Q8gf58 zymomonas m
439	3	10.3	32	3	Q01058	Q01058 kluyveromyc
440	3	10.3	32	3	Q8TGT3	Q8tgt3 saccharomyc
441	3	10.3	32	4	Q12900	Q12900 homo sapien
442	3	10.3	32	4	Q8TC25	Q8tc25 homo sapien
443	3	10.3	32	4	Q96GM7	Q96gm7 homo sapien
444	3	10.3	32	4	Q9HAX8	Q9hax8 homo sapien
445	3	10.3	32	4	Q8TBQ3	Q8tbq3 homo sapien
446	3	10.3	32	4	Q96I20	Q96i20 homo sapien
447	3	10.3	32	4	Q9UN69	Q9un69 homo sapien
448	3	10.3	32	4	Q9UQV1	Q9uqv1 homo sapien
449	3	10.3	32	5	Q9GPD9	Q9gpd9 drosophila
450	3	10.3	32	5	Q8T382	Q8t382 leishmania
451	3	10.3	32	5	O96634	O96634 trypanosoma
452	3	10.3	32	5	Q9TWR8	Q9twr8 procambarus
453	3	10.3	32	5	O18606	O18606 branchiosto
454	3	10.3	32	5	Q8T757	Q8t757 branchiosto
455	3	10.3	32	6	Q9TR67	Q9tr67 sus scrofa
456	3	10.3	32	6	Q8MJ91	Q8mj91 macaca mula

457	3	10.3	32	7	Q8SNF1	Q8snf1 gallinago m
458	3	10.3	32	7	O19722	O19722 homo sapien
459	3	10.3	32	8	Q36494	Q36494 farfantepen
460	3	10.3	32	8	Q8SL89	Q8sl89 euglena ste
461	3	10.3	32	8	Q9GF95	Q9gf95 cercidiphyl
462	3	10.3	32	8	Q31736	Q31736 beta vulgar
463	3	10.3	32	8	Q8SL87	Q8sl87 euglena vir
464	3	10.3	32	8	Q31735	Q31735 beta vulgar
465	3	10.3	32	8	Q9MNM0	Q9mnm0 bufo andrew
466	3	10.3	32	8	Q9MNL0	Q9mnl0 bufo danate
467	3	10.3	32	8	Q951Q4	Q951q4 renilla ren
468	3	10.3	32	8	Q9GF72	Q9gf72 saururus ce
469	3	10.3	32	9	Q9MBU5	Q9mbu5 chlamydia p
470	3	10.3	32	10	Q8S527	Q8s527 ipomoea bat
471	3	10.3	32	10	Q8RXQ5	Q8rxq5 arabidopsis
472	3	10.3	32	10	Q40727	Q40727 oryza sativ
473	3	10.3	32	11	Q9JIU1	Q9jiu1 rattus norv
474	3	10.3	32	11	Q9R0E3	Q9r0e3 mus musculu
475	3	10.3	32	11	Q9QWM2	Q9qwm2 mus musculu
476	3	10.3	32	11	Q9QWB2	Q9qwb2 rattus sp.
477	3	10.3	32	11	Q8C2N8	Q8c2n8 mus musculu
478	3	10.3	32	11	Q8BS12	Q8bs12 mus musculu
479	3	10.3	32	12	Q9WNI5	Q9wni5 tt virus. o
480	3	10.3	32	12	Q914F9	Q914f9 sulfolobus
481	3	10.3	32	12	Q8QYT4	Q8qyt4 grapevine v
482	3	10.3	32	12	Q8QYT7	Q8qyt7 grapevine v
483	3	10.3	32	12	Q8QYU0	Q8qyu0 grapevine v
484	3	10.3	32	12	Q9Q934	Q9q934 shope fibro
485	3	10.3	32	13	Q8QG73	Q8qg73 oncorhynchu
486	3	10.3	32	13	Q8QG72	Q8qg72 salmo salar
487	3	10.3	32	13	Q8QG71	Q8qg71 oncorhynchu
488	3	10.3	32	13	Q9PS21	Q9ps21 carassius a
489	3	10.3	32	13	Q8QG84	Q8qg84 oncorhynchu
490	3	10.3	32	13	Q8QG83	Q8qg83 oncorhynchu
491	3	10.3	32	13	Q8QG82	Q8qg82 oncorhynchu
492	3	10.3	32	13	Q8QG70	Q8qg70 salvelinus
493	3	10.3	32	13	P82780	P82780 rana catesb
494	3	10.3	32	13	Q9W7P3	Q9w7p3 morone saxa
495	3	10.3	32	13	Q9W7P2	Q9w7p2 morone saxa
496	3	10.3	32	16	O50706	O50706 borrelia bu
497	3	10.3	32	16	O50851	O50851 borrelia bu
498	3	10.3	32	16	O50865	O50865 borrelia bu
499	3	10.3	32	16	O51003	O51003 borrelia bu
500	3	10.3	32	16	Q9PGT0	Q9pgt0 xylella fas
501	3	10.3	32	16	Q9KTV2	Q9ktv2 vibrio chol
502	3	10.3	32	16	Q9KPN9	Q9kpn9 vibrio chol
503	3	10.3	32	16	Q9KLF0	Q9klf0 vibrio chol
504	3	10.3	32	16	Q9K7B0	Q9k7b0 bacillus ha
505	3	10.3	32	16	Q9A2H0	Q9a2h0 caulobacter
506	3	10.3	32	16	Q98AB6	Q98ab6 rhizobium l
507	3	10.3	32	16	Q8X3V6	Q8x3v6 escherichia
508	3	10.3	32	16	Q8KG49	Q8kg49 chlorobium
509	3	10.3	32	16	Q8KEZ9	Q8kez9 chlorobium
510	3	10.3	32	16	Q8KCV3	Q8kcv3 chlorobium
511	3	10.3	32	16	Q9K4G0	Q9k4g0 streptomyce
512	3	10.3	32	16	Q8EAD5	Q8ead5 shewanella
513	3	10.3	32	16	Q8CU60	Q8cu60 staphylococ

514	3	10.3	32	16	Q8CTR7	Q8ctr7 staphylococ
515	3	10.3	32	16	Q8CRE7	Q8cre7 staphylococ
516	3	10.3	32	17	Q9HSZ0	Q9hsz0 halobacteri
517	3	10.3	32	17	Q8ZZF7	Q8zzf7 pyrobaculum
518	3	10.3	33	1	Q9UWL4	Q9uwl4 methanopyru
519	3	10.3	33	2	Q8KH96	Q8kh96 pseudomonas
520	3	10.3	33	2	Q9S624	Q9s624 prochloroco
521	3	10.3	33	2	Q9R2M3	Q9r2m3 prochloroco
522	3	10.3	33	2	Q9X3M5	Q9x3m5 prochloroco
523	3	10.3	33	2	Q9S651	Q9s651 streptococc
524	3	10.3	33	2	Q9K370	Q9k370 rhizobium l
525	3	10.3	33	2	Q9S3N5	Q9s3n5 bacillus ce
526	3	10.3	33	2	Q8KQ80	Q8kq80 vibrio chol
527	3	10.3	33	2	Q56414	Q56414 escherichia
528	3	10.3	33	2	Q9S622	Q9s622 prochloroco
529	3	10.3	33	2	Q9F1F4	Q9f1f4 enterococcu
530	3	10.3	33	2	Q9KI23	Q9ki23 helicobacte
531	3	10.3	33	2	Q8GQU2	Q8gqu2 leptospira
532	3	10.3	33	3	Q8TGR1	Q8tgr1 saccharomyc
533	3	10.3	33	4	Q99950	Q99950 homo sapien
534	3	10.3	33	4	Q9UP36	Q9up36 homo sapien
535	3	10.3	33	4	Q15285	Q15285 homo sapien
536	3	10.3	33	4	Q9UDI1	Q9udi1 homo sapien
537	3	10.3	33	4	Q9P1T8	Q9p1t8 homo sapien
538	3	10.3	33	4	Q9BV16	Q9bv16 homo sapien
539	3	10.3	33	4	Q92668	Q92668 homo sapien
540	3	10.3	33	5	Q9GTB2	Q9gtb2 eimeria ten
541	3	10.3	33	5	Q9GT93	Q9gt93 cryptospori
542	3	10.3	33	5	Q26673	Q26673 tethya aura
543	3	10.3	33	5	Q26672	Q26672 tethya aura
544	3	10.3	33	5	Q9GTC2	Q9gtc2 plasmodium
545	3	10.3	33	5	Q27637	Q27637 drosophila
546	3	10.3	33	5	Q9GTB3	Q9gtb3 eimeria ten
547	3	10.3	33	5	Q9GTA6	Q9gta6 sarcocystis
548	3	10.3	33	5	Q9GTA1	Q9gta1 babesia bov
549	3	10.3	33	5	Q17293	Q17293 cancer ante
550	3	10.3	33	5	Q27310	Q27310 paramecium
551	3	10.3	33	5	Q9GTA9	Q9gta9 sarcocystis
552	3	10.3	33	5	O17147	O17147 echinococcu
553	3	10.3	33	5	Q9GT95	Q9gt95 cryptospori
554	3	10.3	33	5	Q9GTA2	Q9gta2 babesia bov
555	3	10.3	33	6	Q28788	Q28788 papio hamad
556	3	10.3	33	6	O18916	O18916 sus scrofa
557	3	10.3	33	6	Q9TSX7	Q9tsx7 sus scrofa
558	3	10.3	33	6	Q95M05	Q95m05 bos taurus
559	3	10.3	33	7	Q8MGU2	Q8mgu2 bos taurus
560	3	10.3	33	7	Q8SNF0	Q8snf0 gallinago m
561	3	10.3	33	8	Q9BAC6	Q9bac6 euglena gra
562	3	10.3	33	8	Q8W9G0	Q8w9g0 meloidogyne
563	3	10.3	33	8	Q9BAC1	Q9bac1 euglena ste
564	3	10.3	33	8	Q9XNP3	Q9xnp3 boophilus m
565	3	10.3	33	8	O78857	O78857 phytophthor
566	3	10.3	33	8	Q9T2N1	Q9t2n1 nicotiana t
567	3	10.3	33	8	Q9BAC4	Q9bac4 euglena mut
568	3	10.3	33	8	Q8WEJ5	Q8wej5 ginkgo bilo
569	3	10.3	33	8	Q8HUH3	Q8huh3 chlamydomon
570	3	10.3	33	8	Q8HS33	Q8hs33 hydrastis c

571	3	10.3	33	9	Q38588	Q38588 bacterioph
572	3	10.3	33	9	Q38551	Q38551 bacterioph
573	3	10.3	33	10	Q49775	Q49775 arabidopsis
574	3	10.3	33	10	Q9S8V5	Q9s8v5 zea mays (m
575	3	10.3	33	10	Q9AYQ5	Q9ayq5 cucumis sat
576	3	10.3	33	11	Q9QVM2	Q9qvm2 mus sp. glu
577	3	10.3	33	12	Q72982	Q72982 hepatitis c
578	3	10.3	33	12	Q73068	Q73068 hepatitis c
579	3	10.3	33	12	Q90085	Q90085 human papil
580	3	10.3	33	12	Q72979	Q72979 hepatitis c
581	3	10.3	33	12	Q91J04	Q91j04 tt virus. o
582	3	10.3	33	12	Q72996	Q72996 hepatitis c
583	3	10.3	33	12	Q91J14	Q91j14 tt virus. o
584	3	10.3	33	12	Q72988	Q72988 hepatitis c
585	3	10.3	33	12	Q72992	Q72992 hepatitis c
586	3	10.3	33	12	Q91J12	Q91j12 tt virus. o
587	3	10.3	33	12	Q91J15	Q91j15 tt virus. o
588	3	10.3	33	12	Q91J07	Q91j07 tt virus. o
589	3	10.3	33	12	Q72995	Q72995 hepatitis c
590	3	10.3	33	12	Q91J09	Q91j09 tt virus. o
591	3	10.3	33	12	Q72990	Q72990 hepatitis c
592	3	10.3	33	12	Q73010	Q73010 hepatitis c
593	3	10.3	33	12	Q86912	Q86912 hepatitis c
594	3	10.3	33	12	Q8V5G7	Q8v5g7 hepatitis c
595	3	10.3	33	12	Q72981	Q72981 hepatitis c
596	3	10.3	33	12	Q91J08	Q91j08 tt virus. o
597	3	10.3	33	12	Q72997	Q72997 hepatitis c
598	3	10.3	33	12	Q73008	Q73008 hepatitis c
599	3	10.3	33	12	Q83963	Q83963 avian influ
600	3	10.3	33	12	Q72986	Q72986 hepatitis c
601	3	10.3	33	12	Q72993	Q72993 hepatitis c
602	3	10.3	33	12	Q91J06	Q91j06 tt virus. o
603	3	10.3	33	12	Q72984	Q72984 hepatitis c
604	3	10.3	33	12	Q73005	Q73005 hepatitis c
605	3	10.3	33	12	Q73067	Q73067 hepatitis c
606	3	10.3	33	12	Q72985	Q72985 hepatitis c
607	3	10.3	33	12	Q72999	Q72999 hepatitis c
608	3	10.3	33	12	Q91J16	Q91j16 tt virus. o
609	3	10.3	33	12	Q72998	Q72998 hepatitis c
610	3	10.3	33	12	Q91J11	Q91j11 tt virus. o
611	3	10.3	33	12	Q72994	Q72994 hepatitis c
612	3	10.3	33	12	Q8V5H0	Q8v5h0 hepatitis c
613	3	10.3	33	12	Q91J13	Q91j13 tt virus. o
614	3	10.3	33	12	Q8V5G8	Q8v5g8 hepatitis c
615	3	10.3	33	12	Q72983	Q72983 hepatitis c
616	3	10.3	33	12	Q73007	Q73007 hepatitis c
617	3	10.3	33	12	Q91J10	Q91j10 tt virus. o
618	3	10.3	33	12	Q72987	Q72987 hepatitis c
619	3	10.3	33	12	Q91J17	Q91j17 tt virus. o
620	3	10.3	33	12	Q69461	Q69461 human herpe
621	3	10.3	33	12	Q8V5G9	Q8v5g9 hepatitis c
622	3	10.3	33	12	Q72978	Q72978 hepatitis c
623	3	10.3	33	12	Q73009	Q73009 hepatitis c
624	3	10.3	33	12	Q73004	Q73004 hepatitis c
625	3	10.3	33	12	Q99138	Q99138 avian influ
626	3	10.3	33	13	P82740	P82740 rana tempor
627	3	10.3	33	13	P82236	P82236 rana tempor

628	3	10.3	33	15	Q9DZ98	Q9dz98 human immun
629	3	10.3	33	15	Q86107	Q86107 simian sarc
630	3	10.3	33	16	Q9PA23	Q9pa23 xylella fas
631	3	10.3	33	16	Q9KQP4	Q9kqp4 vibrio chol
632	3	10.3	33	16	Q9KML1	Q9kml1 vibrio chol
633	3	10.3	33	16	Q97T91	Q97t91 streptococc
634	3	10.3	33	16	Q97PC1	Q97pc1 streptococc
635	3	10.3	33	16	Q932N2	Q932n2 staphylococ
636	3	10.3	33	16	Q8ZKL2	Q8zkl2 salmonella
637	3	10.3	33	16	Q8Z1V4	Q8z1v4 salmonella
638	3	10.3	33	16	Q8U5M4	Q8u5m4 agrobacteri
639	3	10.3	33	16	Q8VK01	Q8vk01 mycobacteri
640	3	10.3	33	16	Q8NUL1	Q8nul1 staphylococ
641	3	10.3	33	16	Q8NT95	Q8nt95 corynebacte
642	3	10.3	33	16	Q8NLP2	Q8nlp2 corynebacte
643	3	10.3	33	16	Q8KG99	Q8kg99 chlorobium
644	3	10.3	33	16	Q8KBZ0	Q8kbz0 chlorobium
645	3	10.3	33	16	Q8G0U8	Q8g0u8 brucella su
646	3	10.3	33	16	Q8FZ67	Q8fz67 brucella su
647	3	10.3	33	16	Q8FYR6	Q8fyr6 brucella su
648	3	10.3	33	16	Q8FY86	Q8fy86 brucella su
649	3	10.3	33	16	Q8FSG0	Q8fsg0 corynebacte
650	3	10.3	33	16	Q8EJH6	Q8ejh6 shewanella
651	3	10.3	33	16	Q8EGA9	Q8ega9 shewanella
652	3	10.3	33	16	Q8EE59	Q8ee59 shewanella
653	3	10.3	33	16	Q8EE42	Q8ee42 shewanella
654	3	10.3	33	16	Q8E8W4	Q8e8w4 shewanella
655	3	10.3	33	16	Q8E1Y5	Q8ely5 streptococc
656	3	10.3	33	16	Q8CTR8	Q8ctr8 staphylococ
657	3	10.3	33	16	Q8CQY7	Q8cqy7 staphylococ
658	3	10.3	33	17	Q9HSX6	Q9hsx6 halobacteri
659	3	10.3	33	17	Q8U2X8	Q8u2x8 pyrococcus
660	3	10.3	34	2	Q54427	Q54427 spiroplasma
661	3	10.3	34	2	Q9X3L6	Q9x3l6 prochloroco
662	3	10.3	34	2	Q9R5U1	Q9r5u1 campylobact
663	3	10.3	34	2	Q44208	Q44208 pseudomonas
664	3	10.3	34	2	Q9X7J6	Q9x7j6 pseudomonas
665	3	10.3	34	2	Q8KYH2	Q8kyh2 bacillus an
666	3	10.3	34	2	O31061	O31061 butyrivibri
667	3	10.3	34	2	Q9R8A2	Q9r8a2 chlamydia t
668	3	10.3	34	2	Q9RZW6	Q9rzw6 borrelia bu
669	3	10.3	34	2	Q8GJC8	Q8gjc8 campylobact
670	3	10.3	34	2	Q8G8C9	Q8g8c9 pseudomonas
671	3	10.3	34	3	Q00377	Q00377 coccidioid
672	3	10.3	34	4	Q99910	Q99910 homo sapien
673	3	10.3	34	4	Q9H3R8	Q9h3r8 homo sapien
674	3	10.3	34	4	Q9UI64	Q9ui64 homo sapien
675	3	10.3	34	4	Q8WY57	Q8wy57 homo sapien
676	3	10.3	34	4	Q8WW51	Q8ww51 homo sapien
677	3	10.3	34	4	Q9BSP7	Q9bsp7 homo sapien
678	3	10.3	34	4	Q9H4L8	Q9h4l8 homo sapien
679	3	10.3	34	4	Q8NEQ3	Q8neq3 homo sapien
680	3	10.3	34	4	Q15251	Q15251 homo sapien
681	3	10.3	34	4	Q9NQY9	Q9nqy9 homo sapien
682	3	10.3	34	5	Q9BIP7	Q9bip7 cooperia pu
683	3	10.3	34	5	Q27821	Q27821 trichomonas
684	3	10.3	34	5	Q9GQE5	Q9gqe5 branchiosto

685	3	10.3	34	6	Q9TS91	Q9ts91 oryctolagus
686	3	10.3	34	6	P79429	P79429 capra hircu
687	3	10.3	34	6	Q9TRI2	Q9tri2 sus scrofa
688	3	10.3	34	6	P82908	P82908 bos taurus
689	3	10.3	34	8	O79025	O79025 enallagma v
690	3	10.3	34	8	Q9T2T7	Q9t2t7 bos taurus
691	3	10.3	34	8	Q8MCA2	Q8mca2 phaseolus a
692	3	10.3	34	8	Q8HKE1	Q8hke1 rhipicephal
693	3	10.3	34	10	Q8W2H0	Q8w2h0 paspalum no
694	3	10.3	34	10	Q8VWL0	Q8vwl0 paspalum no
695	3	10.3	34	10	Q9SCA3	Q9sca3 lycopersico
696	3	10.3	34	11	Q923Z1	Q923z1 mus musculu
697	3	10.3	34	11	Q8R557	Q8r557 mus musculu
698	3	10.3	34	11	Q9ET72	Q9et72 mus musculu
699	3	10.3	34	11	Q99KM9	Q99km9 mus musculu
700	3	10.3	34	11	Q99KX7	Q99kx7 mus musculu
701	3	10.3	34	11	Q8VHL4	Q8vhl4 rattus norv
702	3	10.3	34	11	Q8C4P4	Q8c4p4 mus musculu
703	3	10.3	34	13	O42521	O42521 scyliorhinu
704	3	10.3	34	13	O13101	O13101 ambystoma m
705	3	10.3	34	13	Q8QGG2	Q8qgg2 oncorhynchu
706	3	10.3	34	13	Q8QFM9	Q8qfm9 oncorhynchu
707	3	10.3	34	13	O42526	O42526 scyliorhinu
708	3	10.3	34	13	Q9PRE7	Q9pre7 oryzias lat
709	3	10.3	34	13	Q8QGG1	Q8qgg1 oncorhynchu
710	3	10.3	34	13	Q8QGF7	Q8qgf7 oncorhynchu
711	3	10.3	34	13	Q98TM8	Q98tm8 platichthys
712	3	10.3	34	15	O40445	O40445 human immun
713	3	10.3	34	15	Q9WR32	Q9wr32 human immun
714	3	10.3	34	15	Q9W8Y1	Q9w8y1 chimpanzee
715	3	10.3	34	16	O50812	O50812 borrelia bu
716	3	10.3	34	16	O50877	O50877 borrelia bu
717	3	10.3	34	16	Q9PGH3	Q9pgh3 xylella fas
718	3	10.3	34	16	Q9PGF8	Q9pgf8 xylella fas
719	3	10.3	34	16	Q9PDD0	Q9pdd0 xylella fas
720	3	10.3	34	16	Q9KRA8	Q9kra8 vibrio chol
721	3	10.3	34	16	Q9KPW9	Q9kpw9 vibrio chol
722	3	10.3	34	16	Q9KM63	Q9km63 vibrio chol
723	3	10.3	34	16	Q9K7C6	Q9k7c6 bacillus ha
724	3	10.3	34	16	Q9JY24	Q9jy24 neisseria m
725	3	10.3	34	16	Q9JVP3	Q9jvp3 neisseria m
726	3	10.3	34	16	Q9JUR9	Q9jur9 neisseria m
727	3	10.3	34	16	Q98FK5	Q98fk5 rhizobium l
728	3	10.3	34	16	Q97SF7	Q97sf7 streptococc
729	3	10.3	34	16	Q97PI6	Q97pi6 streptococc
730	3	10.3	34	16	Q9K2B9	Q9k2b9 chlamydia p
731	3	10.3	34	16	Q8X4V1	Q8x4v1 escherichia
732	3	10.3	34	16	Q8U5V2	Q8u5v2 agrobacteri
733	3	10.3	34	16	Q8VIY1	Q8viy1 mycobacteri
734	3	10.3	34	16	Q8RIC7	Q8ric7 fusobacteri
735	3	10.3	34	16	Q8NWX3	Q8nwx3 staphylococ
736	3	10.3	34	16	Q8NV10	Q8nv10 staphylococ
737	3	10.3	34	16	Q8KEQ8	Q8keq8 chlorobium
738	3	10.3	34	16	Q8KEL5	Q8kel5 chlorobium
739	3	10.3	34	16	Q8KDE4	Q8kde4 chlorobium
740	3	10.3	34	16	Q8F830	Q8f830 leptospira
741	3	10.3	34	16	Q8F827	Q8f827 leptospira

742	3	10.3	34	16	Q8F5Y7	Q8f5y7 leptospira
743	3	10.3	34	16	Q8F0V9	Q8f0v9 leptospira
744	3	10.3	34	16	Q8EZR6	Q8ezr6 leptospira
745	3	10.3	34	16	Q8EZ37	Q8ez37 leptospira
746	3	10.3	34	16	Q8EYG6	Q8eyg6 leptospira
747	3	10.3	34	16	Q8EXH6	Q8exh6 leptospira
748	3	10.3	34	16	Q8EXA8	Q8exa8 leptospira
749	3	10.3	34	16	Q8EJ65	Q8ej65 shewanella
750	3	10.3	34	16	Q8EI45	Q8ei45 shewanella
751	3	10.3	34	16	Q8EHU5	Q8ehu5 shewanella
752	3	10.3	34	16	Q8E8Y3	Q8e8y3 shewanella
753	3	10.3	34	16	Q8E8W3	Q8e8w3 shewanella
754	3	10.3	34	16	Q8E173	Q8e173 streptococc
755	3	10.3	34	16	Q8CRY3	Q8cry3 staphylococ
756	3	10.3	34	17	Q8U1I1	Q8uli1 pyrococcus
757	3	10.3	35	2	Q9R624	Q9r624 bacillus su
758	3	10.3	35	2	Q9JPG9	Q9jpg9 neisseria m
759	3	10.3	35	2	Q9R625	Q9r625 bacillus su
760	3	10.3	35	2	Q9X3D6	Q9x3d6 prochloroco
761	3	10.3	35	2	Q9R5I3	Q9r5i3 thermoanaer
762	3	10.3	35	2	Q9FCX4	Q9fcx4 clostridium
763	3	10.3	35	2	Q9XBK0	Q9xbk0 bacillus ce
764	3	10.3	35	2	Q53564	Q53564 neisseria g
765	3	10.3	35	2	Q46537	Q46537 bacteroides
766	3	10.3	35	2	Q9ZG35	Q9zg35 chlamydia t
767	3	10.3	35	2	Q9RHG5	Q9rhg5 bacillus ce
768	3	10.3	35	2	Q9R4A1	Q9r4a1 klebsiella
769	3	10.3	35	2	O30661	O30661 vibrio chol
770	3	10.3	35	2	Q9ZG68	Q9zg68 chlamydia t
771	3	10.3	35	2	Q8RKG3	Q8rkg3 clostridium
772	3	10.3	35	2	Q8RIW2	Q8riw2 clostridium
773	3	10.3	35	2	Q9R626	Q9r626 bacillus su
774	3	10.3	35	2	P81927	P81927 lactobacill
775	3	10.3	35	3	Q96UT3	Q96ut3 saccharomyc
776	3	10.3	35	4	Q9BVR9	Q9bvr9 homo sapien
777	3	10.3	35	4	Q13380	Q13380 homo sapien
778	3	10.3	35	4	Q9BS62	Q9bs62 homo sapien
779	3	10.3	35	4	Q13165	Q13165 homo sapien
780	3	10.3	35	4	Q13828	Q13828 homo sapien
781	3	10.3	35	4	Q13264	Q13264 homo sapien
782	3	10.3	35	4	Q9Y634	Q9y634 homo sapien
783	3	10.3	35	4	Q8IU77	Q8iu77 homo sapien
784	3	10.3	35	5	Q27754	Q27754 pisaster oc
785	3	10.3	35	5	Q9U780	Q9u780 boophilus a
786	3	10.3	35	5	Q26372	Q26372 tribolium c
787	3	10.3	35	5	Q9U782	Q9u782 boophilus m
788	3	10.3	35	5	Q9TVJ7	Q9tvj7 boophilus m
789	3	10.3	35	5	Q9U783	Q9u783 boophilus m
790	3	10.3	35	5	Q9U784	Q9u784 boophilus m
791	3	10.3	35	5	Q9U781	Q9u781 boophilus m
792	3	10.3	35	5	Q8IF21	Q8if21 trypanosoma
793	3	10.3	35	6	Q95N74	Q95n74 equus cabal
794	3	10.3	35	6	Q9MZA7	Q9mza7 sus scrofa
795	3	10.3	35	8	Q951Q6	Q951q6 protoptilum
796	3	10.3	35	8	Q8W7S9	Q8w7s9 colpomenia
797	3	10.3	35	8	Q9GF85	Q9gf85 ginkgo bilo
798	3	10.3	35	8	Q8W7T0	Q8w7t0 petalonia b

799	3	10.3	35	8	Q8W7S8	Q8w7s8 petalonia f
800	3	10.3	35	8	Q8WE70	Q8we70 miliaria ca
801	3	10.3	35	8	Q8W7S7	Q8w7s7 scytosiphon
802	3	10.3	35	8	Q9GF98	Q9gf98 ceratophyll
803	3	10.3	35	8	Q95766	Q95766 cerataphis
804	3	10.3	35	8	Q94P82	Q94p82 corallium r
805	3	10.3	35	8	Q8WEJ7	Q8wej7 cycas circi
806	3	10.3	35	8	Q951S7	Q951s7 anthothela
807	3	10.3	35	8	Q951R1	Q951r1 narella nut
808	3	10.3	35	8	Q951S1	Q951s1 corallium k
809	3	10.3	35	8	Q8WII3	Q8wii3 colpomenia
810	3	10.3	35	8	Q951R3	Q951r3 anthomurice
811	3	10.3	35	8	Q8WIH9	Q8wih9 scytosiphon
812	3	10.3	35	8	Q8WIH5	Q8wih5 hydroclathr
813	3	10.3	35	8	Q951S9	Q951s9 protodendro
814	3	10.3	35	8	Q8WII1	Q8wii1 scytosiphon
815	3	10.3	35	8	Q951Q9	Q951q9 narella sp.
816	3	10.3	35	8	Q951S4	Q951s4 paragorgia
817	3	10.3	35	8	Q951R5	Q951r5 corallium s
818	3	10.3	35	10	Q9SPU2	Q9spu2 arabidopsis
819	3	10.3	35	10	Q9MAB1	Q9mab1 arabidopsis
820	3	10.3	35	10	Q9ZUW2	Q9zuw2 arabidopsis
821	3	10.3	35	10	P92971	P92971 arabidopsis
822	3	10.3	35	10	Q9LV08	Q9lv08 arabidopsis
823	3	10.3	35	10	Q9LQ64	Q9lq64 arabidopsis
824	3	10.3	35	10	Q94IS4	Q94is4 pinus radia
825	3	10.3	35	10	Q39297	Q39297 brassica na
826	3	10.3	35	10	Q8RVJ7	Q8rvj7 populus eur
827	3	10.3	35	10	Q9FJ84	Q9fj84 arabidopsis
828	3	10.3	35	10	Q8GUX4	Q8gux4 picea maria
829	3	10.3	35	11	Q63397	Q63397 rattus norv
830	3	10.3	35	11	Q9JLA4	Q9jla4 mus musculu
831	3	10.3	35	11	Q60608	Q60608 mus musculu
832	3	10.3	35	11	Q9QV50	Q9qv50 rattus sp.
833	3	10.3	35	11	Q922H5	Q922h5 mus musculu
834	3	10.3	35	11	Q8BK89	Q8bk89 mus musculu
835	3	10.3	35	12	Q90151	Q90151 bombyx mori
836	3	10.3	35	12	Q65380	Q65380 banana bunc
837	3	10.3	35	12	Q83333	Q83333 murine hepa
838	3	10.3	35	12	O55549	O55549 measles vir
839	3	10.3	35	12	Q8BB50	Q8bb50 human papil
840	3	10.3	35	13	Q90XB5	Q90xb5 xenopus lae
841	3	10.3	35	13	P83224	P83224 oxyuranus m
842	3	10.3	35	13	P83225	P83225 oxyuranus s
843	3	10.3	35	13	P83227	P83227 oxyuranus m
844	3	10.3	35	13	P83228	P83228 oxyuranus s
845	3	10.3	35	13	P83229	P83229 oxyuranus s
846	3	10.3	35	13	P83226	P83226 oxyuranus s
847	3	10.3	35	15	Q75981	Q75981 human immun
848	3	10.3	35	15	Q70328	Q70328 human immun
849	3	10.3	35	15	Q70380	Q70380 human immun
850	3	10.3	35	15	Q70319	Q70319 human immun
851	3	10.3	35	15	Q79465	Q79465 human immun
852	3	10.3	35	15	Q70426	Q70426 human immun
853	3	10.3	35	15	Q9J3S2	Q9j3s2 human immun
854	3	10.3	35	15	O71950	O71950 human immun
855	3	10.3	35	15	Q9IPY2	Q9ipy2 human immun

856	3	10.3	35	15	Q80574	Q80574	human	immun
857	3	10.3	35	15	Q70425	Q70425	human	immun
858	3	10.3	35	15	Q70362	Q70362	human	immun
859	3	10.3	35	15	Q80601	Q80601	human	immun
860	3	10.3	35	15	Q8QDX6	Q8qdx6	human	immun
861	3	10.3	35	15	Q77702	Q77702	human	immun
862	3	10.3	35	15	Q9QFA0	Q9qfa0	human	immun
863	3	10.3	35	15	Q70330	Q70330	human	immun
864	3	10.3	35	15	Q77584	Q77584	human	immun
865	3	10.3	35	15	Q70317	Q70317	human	immun
866	3	10.3	35	15	Q70316	Q70316	human	immun
867	3	10.3	35	15	Q70402	Q70402	human	immun
868	3	10.3	35	15	Q9YM80	Q9ym80	human	immun
869	3	10.3	35	15	Q8QDY0	Q8qdy0	human	immun
870	3	10.3	35	15	Q75970	Q75970	human	immun
871	3	10.3	35	15	Q70409	Q70409	human	immun
872	3	10.3	35	15	Q70325	Q70325	human	immun
873	3	10.3	35	15	Q9YM17	Q9ym17	human	immun
874	3	10.3	35	15	Q79468	Q79468	human	immun
875	3	10.3	35	15	Q9YM96	Q9ym96	human	immun
876	3	10.3	35	15	Q70363	Q70363	human	immun
877	3	10.3	35	15	Q70321	Q70321	human	immun
878	3	10.3	35	15	Q9YM22	Q9ym22	human	immun
879	3	10.3	35	15	Q75990	Q75990	human	immun
880	3	10.3	35	15	Q70323	Q70323	human	immun
881	3	10.3	35	15	Q75989	Q75989	human	immun
882	3	10.3	35	15	Q70428	Q70428	human	immun
883	3	10.3	35	15	Q9YM67	Q9ym67	human	immun
884	3	10.3	35	15	Q77585	Q77585	human	immun
885	3	10.3	35	15	Q70403	Q70403	human	immun
886	3	10.3	35	15	Q70327	Q70327	human	immun
887	3	10.3	35	15	Q77250	Q77250	human	immun
888	3	10.3	35	15	Q75955	Q75955	human	immun
889	3	10.3	35	15	Q9IPY4	Q9ipy4	human	immun
890	3	10.3	35	15	Q70424	Q70424	human	immun
891	3	10.3	35	15	Q77582	Q77582	human	immun
892	3	10.3	35	16	O07593	O07593	bacillus	su
893	3	10.3	35	16	Q9KR18	Q9kr18	vibrio	chol
894	3	10.3	35	16	Q9KNU1	Q9knu1	vibrio	chol
895	3	10.3	35	16	Q9JWX5	Q9jwx5	neisseria	m
896	3	10.3	35	16	Q9JV38	Q9jv38	neisseria	m
897	3	10.3	35	16	Q9A427	Q9a427	caulobacter	
898	3	10.3	35	16	Q9K241	Q9k241	chlamydia	p
899	3	10.3	35	16	Q8XZB7	Q8xzb7	ralstonia	s
900	3	10.3	35	16	Q8KCA6	Q8kca6	chlorobium	
901	3	10.3	35	16	Q8G2D4	Q8g2d4	brucella	su
902	3	10.3	35	16	Q8F9H5	Q8f9h5	leptospira	
903	3	10.3	35	16	Q8F8D4	Q8f8d4	leptospira	
904	3	10.3	35	16	Q8F1W8	Q8f1w8	leptospira	
905	3	10.3	35	16	Q8EYH6	Q8eyh6	leptospira	
906	3	10.3	35	16	Q8EGT2	Q8egt2	shewanella	
907	3	10.3	35	16	Q8EGC0	Q8egc0	shewanella	
908	3	10.3	35	16	Q8EG97	Q8eg97	shewanella	
909	3	10.3	35	16	Q8EEP3	Q8eep3	shewanella	
910	3	10.3	35	16	Q8E9Z1	Q8e9z1	shewanella	
911	3	10.3	35	16	Q8DUY1	Q8duy1	streptococc	
912	3	10.3	35	17	Q9HMP1	Q9hmp1	halobacteri	

913	3	10.3	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
914	3	10.3	36	2	O06954	O06954 salmonella
915	3	10.3	36	2	Q8VTS7	Q8vts7 listeria in
916	3	10.3	36	2	Q9ZG79	Q9zg79 chlamydia t
917	3	10.3	36	2	Q9RHE3	Q9rhe3 pediococcus
918	3	10.3	36	2	Q8VTS5	Q8vts5 listeria we
919	3	10.3	36	2	Q44437	Q44437 agrobacteri
920	3	10.3	36	2	Q9LB55	Q9lb55 helicobacte
921	3	10.3	36	2	Q48507	Q48507 lactococcus
922	3	10.3	36	2	Q99094	Q99094 salmonella
923	3	10.3	36	2	Q9S635	Q9s635 prochloroco
924	3	10.3	36	2	Q8VTR8	Q8vtr8 listeria iv
925	3	10.3	36	2	Q8VTS0	Q8vts0 listeria mo
926	3	10.3	36	2	Q8KYW1	Q8kyw1 uncultured
927	3	10.3	36	2	Q9R4X9	Q9r4x9 azotobacter
928	3	10.3	36	2	Q9R5L0	Q9r5l0 sarcina ven
929	3	10.3	36	2	Q9X3G2	Q9x3g2 prochloroco
930	3	10.3	36	2	Q9R536	Q9r536 sphingomona
931	3	10.3	36	2	Q8GRH1	Q8grh1 pectobacter
932	3	10.3	36	3	Q96W36	Q96w36 ophiostoma
933	3	10.3	36	4	Q9UNV7	Q9unv7 homo sapien
934	3	10.3	36	4	Q9P1E9	Q9ple9 homo sapien
935	3	10.3	36	4	Q9UPB7	Q9upb7 homo sapien
936	3	10.3	36	4	Q8NE47	Q8ne47 homo sapien
937	3	10.3	36	5	Q9GSY9	Q9gsy9 carcinus ma
938	3	10.3	36	5	Q9NGN1	Q9ngn1 strongyloce
939	3	10.3	36	5	Q27730	Q27730 plasmodium
940	3	10.3	36	5	Q9GNP3	Q9gnp3 caenorhabdi
941	3	10.3	36	5	O01333	O01333 caenorhabdi
942	3	10.3	36	5	Q25781	Q25781 plasmodium
943	3	10.3	36	5	Q8ISR7	Q8isr7 spodoptera
944	3	10.3	36	5	Q8IGF5	Q8igf5 drosophila
945	3	10.3	36	6	O97889	O97889 pongo pygma
946	3	10.3	36	6	Q29059	Q29059 sus scrofa
947	3	10.3	36	6	Q9XT44	Q9xt44 pongo pygma
948	3	10.3	36	6	Q9N1C5	Q9n1c5 bos taurus
949	3	10.3	36	6	O97890	O97890 pan troglod
950	3	10.3	36	6	P79428	P79428 capra hircu
951	3	10.3	36	8	O63675	O63675 emberiza pu
952	3	10.3	36	8	Q9GF81	Q9gf81 gnetum gnem
953	3	10.3	36	8	Q9TIE4	Q9tie4 hydrocotyle
954	3	10.3	36	8	Q9TIF1	Q9tif1 bolax gummi
955	3	10.3	36	8	Q9GFA3	Q9gfa3 cabomba car
956	3	10.3	36	8	Q9GF97	Q9gf97 ceratophyll
957	3	10.3	36	8	Q94VL4	Q94vl4 salmo trutt
958	3	10.3	36	8	Q36303	Q36303 musa schizo
959	3	10.3	36	8	Q9TIF0	Q9tif0 klotzschia
960	3	10.3	36	8	Q94NY5	Q94ny5 salmo salar
961	3	10.3	36	8	Q9GF76	Q9gf76 lactoris fe
962	3	10.3	36	8	Q9MSP9	Q9msp9 nymphaea od
963	3	10.3	36	8	Q9TIF3	Q9tif3 eremocharis
964	3	10.3	36	8	Q9GF74	Q9gf74 liriiodendro
965	3	10.3	36	8	Q9TIE2	Q9tie2 aralia chin
966	3	10.3	36	8	Q9TIF2	Q9tif2 azorella tr
967	3	10.3	36	8	Q9GF89	Q9gf89 drimys wint
968	3	10.3	36	8	Q9MSR0	Q9msr0 zamia furfu
969	3	10.3	36	8	O63650	O63650 emberiza sc

970	3	10.3	36	8	Q9TIE3	Q9tie3 hydrocotyle
971	3	10.3	36	8	Q9TIE5	Q9tie5 xanthosia a
972	3	10.3	36	8	Q9GFA9	Q9gfa9 acorus cala
973	3	10.3	36	8	Q8HS50	Q8hs50 ascarina lu
974	3	10.3	36	8	Q8HS46	Q8hs46 austrobaile
975	3	10.3	36	8	Q8HS42	Q8hs42 chloranthus
976	3	10.3	36	8	Q8HS31	Q8hs31 lilium supe
977	3	10.3	36	8	Q8HS27	Q8hs27 magnolia st
978	3	10.3	36	8	Q8HS18	Q8hs18 sagittaria
979	3	10.3	36	8	Q8HKF5	Q8hkf5 rhipicephal
980	3	10.3	36	8	Q8HKC6	Q8hkc6 haemaphysal
981	3	10.3	36	10	Q38977	Q38977 arabidopsis
982	3	10.3	36	10	Q8VY71	Q8vy71 arabidopsis
983	3	10.3	36	10	Q41995	Q41995 arabidopsis
984	3	10.3	36	11	Q60937	Q60937 mus musculu
985	3	10.3	36	11	P97598	P97598 rattus norv
986	3	10.3	36	12	Q9QQS6	Q9qqqs6 tanapox vir
987	3	10.3	36	12	O90722	O90722 calicivirus
988	3	10.3	36	12	Q83609	Q83609 myxoma viru
989	3	10.3	36	12	Q91CY3	Q91cy3 tt virus. o
990	3	10.3	36	12	Q8QQZ2	Q8qqz2 simian viru
991	3	10.3	36	13	O42264	O42264 xenopus lae
992	3	10.3	36	13	Q8QGS0	Q8qgs0 gallus gall
993	3	10.3	36	15	Q90RH5	Q90rh5 human immun
994	3	10.3	36	15	Q76587	Q76587 human immun
995	3	10.3	36	15	Q80551	Q80551 human immun
996	3	10.3	36	15	Q9YNX9	Q9ynx9 human immun
997	3	10.3	36	15	Q80550	Q80550 human immun
998	3	10.3	36	15	Q80553	Q80553 human immun
999	3	10.3	36	15	Q79436	Q79436 human immun
1000	3	10.3	36	15	O40258	O40258 human immun

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382953; AAK63072.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 48.3%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||
Db 14 VSEIQLMHNLGKHL 27

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 48.3%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||
Db 14 VSEIQLMHNLGKHL 27

RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359533; PubMed=8078520;
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;
 RT "Sequence heterogeneity of the echinococcal antigen B.";
 RL Mol. Biochem. Parasitol. 64:171-175(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 17.2%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 15 LRKKL 19

RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007622; AAK79045.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 17.2%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 17.2%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
|||||
Db 26 LRKKL 30

RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK011220; BAC25325.1; -.
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 17.2%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
 |||||
 Db 2 SVSEI 6

RESULT 7
 O24285

ID O24285 PRELIMINARY; PRT; 28 AA.
 AC O24285;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE LFY protein (Fragment).
 GN LFY.
 OS Pinus radiata (Monterey pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vegetative;
 RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
 RT "Partial characterization of Pinus radiata meristem identity homolog
 RT gene (LFY).";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U66725; AAB06792.1; -.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 13.8%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 15 LRKK 18

RESULT 8

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.
AC Q8GZQ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SNF-1 related kinase (Fragment).
GN BKIN12.
OS Hordeum vulgare var. distichum (Two-rowed barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=112509;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Igri;
RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;
RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF448389; AAN76447.1; -.
KW Kinase.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 13.8%; Score 4; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
|||
Db 18 NLGK 21

RESULT 9

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.
AC Q49148;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE PQQ biosynthesis polypeptide.
GN PQQD.
OS Methylobacterium extorquens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Methylobacteriaceae; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AM1;
RX MEDLINE=94179111; PubMed=8132470;

RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of *Methylobacterium extorquens* AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 13.8%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 8 VSEI 11

RESULT 10

Q9UCL2

ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
 AC Q9UCL2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Renal intestinal-type alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatase.
 DR ProDom; PD001868; Alk_phosphatase; 1.
 SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BEEAD8D0 CRC64;

Query Match 13.8%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 23 KKLQ 26

RESULT 11

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.
 AC Q96PP3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).
 GN SPINK5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,
 RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,
 RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,
 RA Uitto J., Hovnanian A., Richard G.;
 RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with
 RT Netherton syndrome - Implications for mutation detection and first
 RT case of prenatal diagnosis."
 RL J. Invest. Dermatol. 0:0-0(2001).
 DR EMBL; AF295783; AAK97140.1; -.
 FT NON_TER 1 1
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 13.8%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 14 NLGK 17

RESULT 12

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.
 AC Q25603;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Tubulin.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chandrashekar R., Curtis K.C., Weil G.J.;
 RT "Onchocerca volvulus cDNA clone."
 RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U15095; AAA50364.1; -.
 SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 13.8%; Score 4; DB 5; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||

Db 4 VSEI 7

RESULT 13

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.
AC O13043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268658; PubMed=9108066;
RA Schlake T., Schorpp M., Nehls M., Boehm T.;
RT "The nude gene encodes a sequence-specific DNA binding protein with
RT homologs in organisms that lack an anticipatory immune system.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
DR EMBL; Y11539; CAA72302.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR ProDom; PD000425; TF_Fork_head; 1.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 13.8%; Score 4; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 17 VSEI 20

RESULT 14

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.
AC Q9JMV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Luciferase alpha-subunit (Fragment).
GN LUXA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;

RA Lotz W., Bauer T.;
 RT "luxAB/kan-cassette for site-directed insertion mutagenesis and
 RT bacterial transcription studies."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RA Olsson O., Koncz C., Szalay A.;
 RT "The use of luxA gene of the bacterial luciferase operon as a reporter
 RT gene."
 RL Mol. Gen. Genet. 215:1-9(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RX MEDLINE=92114868; PubMed=1685011;
 RA Escher A., O'Kane D.J., Szalay A.;
 RT "The beta subunit polypeptide of Vibrio harveyi luciferase determines
 RT light emission at 42 degrees C."
 RL Mol. Gen. Genet. 230:385-393(1991).
 DR EMBL; AJ249443; CAB96206.1; -.
 DR HSSP; P07740; 1LUC.
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 13.8%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 26 NLGK 29

RESULT 15

Q9UBV5

ID Q9UBV5 PRELIMINARY; PRT; 30 AA.
 AC Q9UBV5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Intestinal alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney."
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatse.
 DR ProDom; PD001868; Alk_phosphatse; 1.

SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BEB9BDE6 CRC64;

Query Match 13.8%; Score 4; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 24 KKLQ 27

RESULT 16

Q8DZP7

ID Q8DZP7 PRELIMINARY; PRT; 30 AA.
AC Q8DZP7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SAG1053.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014240; AAM99934.1; -.
DR TIGR; SAG1053; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 13.8%; Score 4; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 23 KKLQ 26

RESULT 17

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.

AC Q55314;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Urf2 protein (Fragment).
 GN URF2.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96085144; PubMed=8521845;
 RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
 RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate
 RT dehydrogenase genes from the thermophilic archaeon Sulfolobus
 RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and
 RT expression on Escherichia coli.";
 RL Eur. J. Biochem. 233:800-808(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94082761; PubMed=8259927;
 RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;
 RT "Nucleotide sequence and molecular evolution of the gene coding for
 RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
 RT archaeobacterium Sulfolobus solfataricus.";
 RL Biochem. Genet. 31:241-251(1993).
 DR EMBL; X80178; CAA56461.1; -.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 13.8%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 WLRK 26
 ||||
 Db 11 WLRK 14

RESULT 18

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
 AC Q8NEI8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC030993; AAH30993.1; -.

KW Hypothetical protein.

FT NON_TER 1 1

SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 13.8%; Score 4; DB 4; Length 31;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5

||||

Db 18 VSEI 21

RESULT 19

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.

AC Q9MS77;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Photosystem I protein M.

GN PSAM.

OS Phacus acuminata.

OG Chloroplast.

OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.

OX NCBI_TaxID=130316;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21080550; PubMed=11212923;

RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;

RT "Comparison of psbK operon organization and group III intron content

RT in chloroplast genomes of 12 Euglenoid species.";

RL Mol. Gen. Genet. 264:682-690(2001).

DR EMBL; AF241276; AAF82438.1; -.

KW Chloroplast.

SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 13.8%; Score 4; DB 8; Length 31;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13

||||

Db 24 NLGK 27

RESULT 20

O50669

ID O50669 PRELIMINARY; PRT; 31 AA.

AC O50669;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein BBH11.

GN BBH11.

OS Borrelia burgdorferi (Lyme disease spirochete).

OG Plasmid lp28-3.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";
 RL Nature 390:580-586(1997).
 DR EMBL; AE000784; AAC66002.1; -.
 DR TIGR; BBH11; -.
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 13.8%; Score 4; DB 16; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 26 KKLQ 29

RESULT 21

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.
 AC Q9QZQ2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Neurotensin receptor (Fragment).
 GN NTSR OR NTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=99445567; PubMed=10514493;
 RA Tavares D., Tully K., Dobner P.R.;
 RT "Sequences required for induction of neurotensin receptor gene
 RT expression during neuronal differentiation of N1E-115 neuroblastoma
 RT cells.";
 RL J. Biol. Chem. 274:30066-30079(1999).
 DR EMBL; AF172326; AAD51806.1; -.
 DR MGD; MGI:97386; Ntsr.
 KW Receptor.

FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 13.8%; Score 4; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
|||
Db 2 HLNS 5

RESULT 22

Q95SD4

ID Q95SD4 PRELIMINARY; PRT; 33 AA.
AC Q95SD4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM02640p.
GN BCDNA:GM02640.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY060847; AAL28395.1; -.
DR FlyBase; FBgn0047288; BcdNA:GM02640.
SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBE4A7 CRC64;

Query Match 13.8%; Score 4; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 21 KKLQ 24

RESULT 23

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
AC Q9PKX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein TC0337.
GN TC0337.
OS Chlamydia muridarum.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MoPn / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002301; AAF39200.1; -.
 DR TIGR; TC0337; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 13.8%; Score 4; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 26 LRKK 29

RESULT 24

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
 AC Q9ZG81;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE ATP-dependent permease (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087260; AAD04038.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 13.8%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||

Db 25 LRKK 28

RESULT 25

Q8GFK2

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
AC Q8GFK2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ORF37.
OS Staphylococcus aureus.
OG Plasmid EDINA plasmid.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-1;
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
RT plasmid.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP003089; BAC54529.1; -.
KW Plasmid.
SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 13.8%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 6 KKLQ 9

RESULT 26

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
AC Q90ZJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain long form (Fragment).
GN PDGF-A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363439; PubMed=11470524;
RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
RT "Characterization and expression of three forms of cDNA encoding
RT chicken platelet-derived growth factor-A chain.";
RL Gene 272:181-190(2001).
DR EMBL; AB031024; BAB62544.1; -.

FT NON_TER 1 1
SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 13.8%; Score 4; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
|||
Db 28 RKKL 31

RESULT 27

Q8G2Q2

ID Q8G2Q2 PRELIMINARY; PRT; 34 AA.
AC Q8G2Q2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN BR0266.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014339; AAN29215.1; -.
DR TIGR; BR0266; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 3781 MW; 76E820326E6CA66E CRC64;

Query Match 13.8%; Score 4; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGKH 14
|||
Db 10 LGKH 13

RESULT 28

Q8V6J8

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
AC Q8V6J8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 4.1 kDa protein.
 OS Halovirus HF2.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OX NCBI_TaxID=33771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyll-Smith M.L.;
 RT "Sequence and transcription of halovirus HF2."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF222060; AAL55025.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 35 AA; 4115 MW; 2652C319622E9CE4 CRC64;

Query Match 13.8%; Score 4; DB 12; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
 Db 10 SVSE 13

RESULT 29

Q9KQG4

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.
 AC Q9KQG4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein VC2034.
 GN VC2034.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL; AE004278; AAF95182.1; -.
 DR TIGR; VC2034; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 13.8%; Score 4; DB 16; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 24 KKLQ 27

RESULT 30

Q97RG6

ID Q97RG6 PRELIMINARY; PRT; 35 AA.
AC Q97RG6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein SP0853.
GN SP0853.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AE007391; AAK74982.1; -.
DR TIGR; SP0853; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;

Query Match 13.8%; Score 4; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 30 KKLQ 33

RESULT 31

Q8F102

ID Q8F102 PRELIMINARY; PRT; 35 AA.
AC Q8F102;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.
 GN LA3339.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE011494; AAN50536.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 13.8%; Score 4; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
 ||||
 Db 3 HLNS 6

RESULT 32

Q53920

ID Q53920 PRELIMINARY; PRT; 36 AA.
 AC Q53920;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE OrfA protein (Fragment).
 GN ORFA.
 OS Streptomyces chrysomallus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1899;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341259; PubMed=8062824;
 RA Pahl A., Keller U.;
 RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
 RT of two FK506-binding domains with its gene transcriptionally coupled
 RT to the FKBP-12 gene."
 RL EMBO J. 13:3472-3480(1994).
 DR EMBL; Z34523; CAA84281.1; -.
 DR InterPro; IPR004347; DUF245.
 DR Pfam; PF03136; DUF245; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 36 AA; 4121 MW; EBD470AAF99A728E CRC64;

Query Match 13.8%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
 Db 27 ERVE 30

RESULT 33

O68941

ID O68941 PRELIMINARY; PRT; 36 AA.
 AC O68941;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Dinitrogenase 3 beta subunit (Fragment).
 GN ANFK.
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 OX NCBI_TaxID=1085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loveless T.M., Bishop P.E.;
 RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
 RT in Diverse Diazotrophs.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF058778; AAC14327.1; -.
 DR InterPro; IPR000510; Oxred_nitrognsl.
 DR Pfam; PF00148; oxidored_nitro; 1.
 FT NON_TER 36 36
 SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFD437D97 CRC64;

Query Match 13.8%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 5 LRKK 8

RESULT 34

Q8WXW8

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.
 AC Q8WXW8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Urea transporter JK glycoprotein (Fragment).
 GN JK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;
 RT "Molecular Basis of the Jk(a-b-) Phenotype in Non-Finnish European
 RT Pedigrees.";
 RL Br. J. Haematol. 0:0-0(2001).
 DR EMBL; AF328890; AAL37474.1; -.
 DR InterPro; IPR004937; Urea_transporter.

DR Pfam; PF03253; UT; 1.
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 13.8%; Score 4; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNSM 18
|||
Db 7 LNSM 10

RESULT 35

Q9SJ63

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.
AC Q9SJ63;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE At2g35870 protein.
GN AT2G35870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC007017; AAD21470.1; -.
SQ SEQUENCE 36 AA; 4358 MW; DC966779BBD6B834 CRC64;

Query Match 13.8%; Score 4; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 4 KKLQ 7

RESULT 36

Q9PXD1

ID Q9PXD1 PRELIMINARY; PRT; 36 AA.
 AC Q9PXD1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
 DE (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96343121; PubMed=8750162;
 RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
 RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.;
 RT "Genotype, slow decrease in virus titer during interferon treatment
 RT and high degree of sequence variability of hypervariable region are
 RT indicative of poor response to interferon treatment in patients with
 RT chronic hepatitis type C.";
 RL J. Hepatol. 23:648-653(1995).
 DR InterPro; IPR002531; HCV_NS1.
 DR Pfam; PF01560; HCV_NS1; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 13.8%; Score 4; DB 12; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQLM 8
 ||||
 Db 33 IQLM 36

RESULT 37

Q91D77

ID Q91D77 PRELIMINARY; PRT; 36 AA.
 AC Q91D77;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF2 hypothetical protein, isolate:HM0319 (Fragment).
 OS TTV-like mini virus.
 OC Viruses; ssDNA viruses; Circoviridae.
 OX NCBI_TaxID=93678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HM0319;
 RA Michitaka K., Matsubara H., Horiike N., Kihana T., Yano M., Mori T.,
 RA Onji M.;
 RT "Existence of TT virus DNA and TTV-like mini virus DNA in infant cord
 RT blood.";

RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB059561; BAB69654.1; -.
DR InterPro; IPR004118; TT_ORF2.
DR Pfam; PF02957; TT_ORF2; 1.
KW Hypothetical protein.
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4291 MW; 92145F475EA841F1 CRC64;

Query Match 13.8%; Score 4; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 14 KKLQ 17

RESULT 38

Q9YHT9

ID Q9YHT9 PRELIMINARY; PRT; 36 AA.
AC Q9YHT9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Synaptosome-associated protein 25.2 (Fragment).
GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99057281; PubMed=9843147;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage."
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091596; AAC73006.1; -.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
FT NON_TER 1 1
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4046 MW; E3434855F7EEC02F CRC64;

Query Match 13.8%; Score 4; DB 13; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 2 ERVE 5

RESULT 39

Q97S91

ID Q97S91 PRELIMINARY; PRT; 36 AA.
AC Q97S91;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein SP0497.
GN SP0497.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AE007361; AAK74655.1; -.
DR TIGR; SP0497; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 36 AA; 4282 MW; 749D427D078ACA76 CRC64;

Query Match 13.8%; Score 4; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 10 KKLQ 13

RESULT 40

Q8KYJ0
ID Q8KYJ0 PRELIMINARY; PRT; 37 AA.
AC Q8KYJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Conserved hypothetical protein.
GN BXA0180.
OS Bacillus anthracis.
OG Plasmid pX01.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2012;
RX MEDLINE=22061436; PubMed=12004073;

RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
RA Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
RA Keim P., Fraser C.M.;
RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
RT Bacillus anthracis.";
RL Science 296:2028-2033(2002).
DR EMBL; AE011190; AAM26125.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 37 AA; 4416 MW; B5B11661AC3522BD CRC64;

Query Match 13.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 11 LRKK 14

Search completed: January 14, 2004, 10:41:59
Job time : 23.6822 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 4.78816 Seconds
 (without alignments)
 284.822 Million cell updates/sec

Title: US-09-843-221A-167
 Perfect score: 29
 Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	17.2	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	13.8	39	1	SR1C_SARPE	P08377 sarcophaga
3	3	10.3	28	1	CH60_MYCSM	P80673 mycobacteri
4	3	10.3	28	1	COXB_SOLTU	P80499 solanum tub
5	3	10.3	28	1	GUN_SCHCO	P81190 schizophyll
6	3	10.3	28	1	PA23_TRIST	P82894 trimeresuru
7	3	10.3	28	1	PA2C_PSEPO	P20260 pseudechis
8	3	10.3	28	1	VI03_VACCP	Q00334 vaccinia vi
9	3	10.3	28	1	VIP_ALLMI	P48142 alligator m
10	3	10.3	28	1	VIP_RANRI	P81016 rana ridibu
11	3	10.3	28	1	VIP_SHEEP	P04565 ovis aries
12	3	10.3	29	1	DMD_RAT	P11530 rattus norv
13	3	10.3	29	1	GALA_ALLMI	P47215 alligator m
14	3	10.3	29	1	GALA_AMICA	P47214 amia calva
15	3	10.3	29	1	GALA_CHICK	P30802 gallus gall
16	3	10.3	29	1	GALA_ONCMY	P47213 oncorhynch
17	3	10.3	29	1	GALA_RANRI	P47216 rana ridibu

18	3	10.3	29	1	GALA_SHEEP	P31234	ovis aries
19	3	10.3	29	1	GLUC_CHIBR	P31297	chinchilla
20	3	10.3	29	1	IPYR_DESVH	P19371	desulfovibr
21	3	10.3	29	1	NUO1_SOLTU	P80267	solanum tub
22	3	10.3	29	1	P2SM_LOXIN	P83046	loxosceles
23	3	10.3	29	1	PCG4_PACGO	P82417	pachycondyl
24	3	10.3	29	1	RS7_METTE	O93639	methanosarc
25	3	10.3	29	1	SODC_OLEEU	P80740	olea europa
26	3	10.3	29	1	TL16_SPIOL	P81834	spinacia ol
27	3	10.3	30	1	DMS3_PHYSA	P80279	phyllomedus
28	3	10.3	30	1	FTN_BACFR	P28733	bacteroides
29	3	10.3	30	1	OTCC_AERPU	P11726	aeromonas p
30	3	10.3	30	1	PCG2_PACGO	P82415	pachycondyl
31	3	10.3	30	1	PCG3_PACGO	P82416	pachycondyl
32	3	10.3	30	1	PSAM_PORPU	P51395	porphyra pu
33	3	10.3	30	1	TX2_THRPR	P83476	thrixopelma
34	3	10.3	30	1	UP61_UPEIN	P82037	uperoleia i
35	3	10.3	30	1	UP62_UPEIN	P82038	uperoleia i
36	3	10.3	30	1	VAA2_EQUAR	Q04238	equisetum a
37	3	10.3	30	1	Y523_BORBU	O51473	borrelia bu
38	3	10.3	31	1	CEC1_PIG	P14661	sus scrofa
39	3	10.3	31	1	CXMA_CONMR	P56708	conus marmo
40	3	10.3	31	1	DEJP_DROME	P81160	drosophila
41	3	10.3	31	1	DIUX_DIPPU	P82372	diploptera
42	3	10.3	31	1	H13_WHEAT	P15872	triticum ae
43	3	10.3	31	1	LPL_BUCRP	Q53017	buchnera ap
44	3	10.3	31	1	MALK_PHOLU	P41124	photorhabdu
45	3	10.3	31	1	PETL_LOTJA	Q9bbr4	lotus japon
46	3	10.3	31	1	PETL_MARPO	P12179	marchantia
47	3	10.3	31	1	PETL_MESVI	Q9mun4	mesostigma
48	3	10.3	31	1	PETL_NEPOL	Q9tky9	nephroselmi
49	3	10.3	31	1	PSAM_EUGGR	P31479	euglena gra
50	3	10.3	31	1	SARL_MOUSE	Q9cqd6	mus musculu
51	3	10.3	31	1	SARL_RABIT	P42532	oryctolagus
52	3	10.3	31	1	SCK5_ANDMA	P31719	androctonus
53	3	10.3	31	1	SCKL_LEIQH	P16341	leiurus qui
54	3	10.3	31	1	Y822_BORBU	O51762	borrelia bu
55	3	10.3	32	1	ADHR_DROYA	P28487	drosophila
56	3	10.3	32	1	CAL2_ONCKE	P01264	oncorhynchu
57	3	10.3	32	1	CAL3_ONCKI	P01265	oncorhynchu
58	3	10.3	32	1	CAL_ANGJA	P01262	anguilla ja
59	3	10.3	32	1	COA2_BPIF1	O80296	bacterioph
60	3	10.3	32	1	CY31_DESAC	P81078	desulfuromo
61	3	10.3	32	1	FF21_SALEN	P55224	salmonella
62	3	10.3	32	1	IAPP_PIG	Q29119	sus scrofa
63	3	10.3	32	1	ITR3_CUCPE	P10293	cucurbita p
64	3	10.3	32	1	ITR4_CUCMA	P07853	cucurbita m
65	3	10.3	32	1	LEC_DOLAX	P02875	dolichos ax
66	3	10.3	32	1	MIFH_TRITR	P81748	trichuris t
67	3	10.3	32	1	P1SM_LOXIN	P83045	loxosceles
68	3	10.3	32	1	PETM_GUIITH	O78499	guillardia
69	3	10.3	32	1	PHSS_DESBN	P13064	desulfovibr
70	3	10.3	32	1	PSAM_MARPO	P31590	marchantia
71	3	10.3	32	1	PSBQ_PEA	P19589	pisum sativ
72	3	10.3	32	1	PSBT_ODOSI	P49516	odontella s
73	3	10.3	32	1	PSBZ_EUGST	Q8sl89	euglena ste
74	3	10.3	32	1	PSBZ_EUGVI	Q8sl87	euglena vir

75	3	10.3	32	1	Y160_BPT4	P39247	bacterioph
76	3	10.3	32	1	YCPG_MASLA	P29735	mastigoclad
77	3	10.3	33	1	GGN1_RANRU	P80395	rana rugosa
78	3	10.3	33	1	RUGB_RANRU	P80955	rana rugosa
79	3	10.3	33	1	T1F_PARTE	Q27172	paramecium
80	3	10.3	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
81	3	10.3	33	1	YC12_EUGGR	P31559	euglena gra
82	3	10.3	34	1	DMS1_PHYSA	P24302	phyllomedus
83	3	10.3	34	1	DMS2_PHYSA	P80278	phyllomedus
84	3	10.3	34	1	GUN1_SCLSC	P21833	sclerotinia
85	3	10.3	34	1	TX1_SCOGR	P56855	scodra gris
86	3	10.3	35	1	CECA_AEDAL	P81417	aedes albop
87	3	10.3	35	1	COPA_CANFA	P40765	canis famil
88	3	10.3	35	1	CPI2_PIG	P80736	sus scrofa
89	3	10.3	35	1	GP58_BPSP1	O48412	bacterioph
90	3	10.3	35	1	LEC1_CYTSE	P22970	cytissus ses
91	3	10.3	35	1	LEC3_ULEEU	P23032	ulex europe
92	3	10.3	35	1	NP30_STAAU	P21222	staphylococ
93	3	10.3	35	1	PETG_CYACA	Q9tlq9	cyanidium c
94	3	10.3	35	1	PSBM_SYNY3	P72701	synechocyst
95	3	10.3	35	1	RL15_SYNP7	P31160	synechococc
96	3	10.3	35	1	SCKK_TITSE	P56219	tityus serr
97	3	10.3	35	1	TX1_GRASP	P56852	grammostola
98	3	10.3	35	1	TX1_THRPR	P83480	thrixopelma
99	3	10.3	35	1	TX2_GRASP	P56853	grammostola
100	3	10.3	35	1	VORB_METTM	P80908	methanobact
101	3	10.3	35	1	YRKM_BACSU	P54440	bacillus su
102	3	10.3	36	1	ELH_THETS	P80594	theromyzon
103	3	10.3	36	1	NPF_ARTTR	P41334	artioposthi
104	3	10.3	36	1	OSTS_YEAST	Q99380	saccharomyc
105	3	10.3	36	1	PETM_SYNY3	P74810	synechocyst
106	3	10.3	36	1	R18A_BOVIN	P82919	bos taurus
107	3	10.3	36	1	RET4_CHICK	P30370	gallus gall
108	3	10.3	36	1	RL6_HALCU	P05968	halobacteri
109	3	10.3	36	1	Y260_BACHD	Q9kg53	bacillus ha
110	3	10.3	36	1	Y609_ARCFU	O29646	archaeoglob
111	3	10.3	37	1	DIU1_TENMO	P56618	tenebrio mo
112	3	10.3	37	1	IAPP_CRIGR	P19890	cricetulus
113	3	10.3	37	1	LCNM_LACLA	P83002	lactococcus
114	3	10.3	37	1	OGT1_RABIT	P81436	oryctolagus
115	3	10.3	37	1	PIP7_BOVIN	P21671	bos taurus
116	3	10.3	37	1	RL36_PASMU	P57942	pasteurella
117	3	10.3	37	1	SCKI_MESTA	P24663	mesobuthus
118	3	10.3	37	1	Y63_BPT3	P20328	bacterioph
119	3	10.3	38	1	CPRP_CANPG	P81033	cancer pagu
120	3	10.3	38	1	DNP_DENAN	P28374	dendroaspis
121	3	10.3	38	1	NLT1_VITSX	P80275	vitis sp. (
122	3	10.3	38	1	NLT2_VITSX	P33556	vitis sp. (
123	3	10.3	38	1	OBP2_HYSCR	P81648	hystrix cri
124	3	10.3	38	1	PYSA_METBA	P80521	methanosarc
125	3	10.3	38	1	RL36_ECOLI	P21194	escherichia
126	3	10.3	38	1	RL36_PSEAE	Q9hwf6	pseudomonas
127	3	10.3	38	1	RL36_THEMA	Q9xli6	thermotoga
128	3	10.3	38	1	RL36_YERPE	Q8zj91	yersinia pe
129	3	10.3	38	1	RR12_PINCO	P49168	pinus conto
130	3	10.3	38	1	YJ39_ARCFU	O28340	archaeoglob
131	3	10.3	39	1	CEC_GLOMR	P83403	glossina mo

132	3	10.3	39	1	COLI_BALPH	P01195	balaenopter
133	3	10.3	39	1	COLI_RABIT	P06297	oryctolagus
134	3	10.3	39	1	COLI_SQUAC	P01197	squalus aca
135	3	10.3	39	1	COLI_STRCA	P01196	struthio ca
136	3	10.3	39	1	EXE3_HELHO	P20394	heloderma h
137	3	10.3	39	1	FUC3_RAT	P80349	rattus norv
138	3	10.3	39	1	H2A_BUFBG	P55897	bufo bufo g
139	3	10.3	39	1	LCGA_LACLA	P36961	lactococcus
140	3	10.3	39	1	PA2_AGKBI	Q9psf9	agkistrodon
141	3	10.3	39	1	PSBX_PORPU	P51197	porphyra pu
142	3	10.3	40	1	ALB1_TRASC	P81188	trachemys s
143	3	10.3	40	1	HPT_RABIT	P19007	oryctolagus
144	3	10.3	40	1	HS9A_RABIT	P30946	oryctolagus
145	3	10.3	40	1	KAD_STACA	P35141	staphylococ
146	3	10.3	40	1	PHRK_BACSU	O31840	bacillus su
147	3	10.3	40	1	PRE_BACLI	P18189	bacillus li
148	3	10.3	40	1	RK33_PEA	P51416	pisum sativ
149	3	10.3	40	1	RRPO_LSV	P27328	lily sympto
150	3	10.3	40	1	SAUV_PHYSA	P01144	phyllomedus
151	3	10.3	40	1	SR1D_SARPE	P18312	sarcophaga
152	3	10.3	40	1	UC11_MAIZE	P80617	zea mays (m
153	3	10.3	40	1	VIT_MELGA	P56531	meleagris g
154	3	10.3	40	1	YDRB_STRPE	P32012	streptomyce
155	2	6.9	28	1	ACON_CANAL	P82611	candida alb
156	2	6.9	28	1	APC1_RABIT	P33047	oryctolagus
157	2	6.9	28	1	ARYC_NOCGL	P80008	nocardia gl
158	2	6.9	28	1	CIQC_RAT	P31722	rattus norv
159	2	6.9	28	1	ETX2_BACCE	P80568	bacillus ce
160	2	6.9	28	1	FIBA_CANFA	P02673	canis famil
161	2	6.9	28	1	FLA1_TREPH	P21988	treponema p
162	2	6.9	28	1	GDO_TRIMO	P02865	triticum mo
163	2	6.9	28	1	GRP_ALLMI	P31886	alligator m
164	2	6.9	28	1	GTS5_CHICK	P20137	gallus gall
165	2	6.9	28	1	GVPC_OSCAG	P80999	oscillator
166	2	6.9	28	1	HORC_HORSP	P02864	hordeum spo
167	2	6.9	28	1	ICPP_VIPLE	P82475	vipera lebe
168	2	6.9	28	1	IEL1_MOMCH	P10296	momordica c
169	2	6.9	28	1	IORB_METTM	P80911	methanobact
170	2	6.9	28	1	ITR2_MOMCH	P10295	momordica c
171	2	6.9	28	1	ITR3_LUFCY	P35628	luffa cylin
172	2	6.9	28	1	ITRA_MOMCH	P30709	momordica c
173	2	6.9	28	1	LECA_IRIHO	P36230	iris hollan
174	2	6.9	28	1	LPFS_ECOLI	P22183	escherichia
175	2	6.9	28	1	LPL_ECOLI	P09149	escherichia
176	2	6.9	28	1	LPL_SALTI	Q8z9h9	salmonella
177	2	6.9	28	1	LPL_SALTY	P03062	salmonella
178	2	6.9	28	1	LPW_SERMA	P03055	serratia ma
179	2	6.9	28	1	MAAI_RAT	P57113	rattus norv
180	2	6.9	28	1	MCDP_MEGPE	P04567	megabombus
181	2	6.9	28	1	NLT2_WHEAT	P39085	triticum ae
182	2	6.9	28	1	NXL1_BOUAN	P34074	boulengerin
183	2	6.9	28	1	OBP1_HYSCR	P81647	hystrix cri
184	2	6.9	28	1	OMPA_YERPS	P38399	yersinia ps
185	2	6.9	28	1	ORND_PLAOR	P25513	placobdella
186	2	6.9	28	1	OST1_CHICK	P80896	gallus gall
187	2	6.9	28	1	PA22_MICNI	P21791	micrurus ni
188	2	6.9	28	1	PA23_MICNI	P21792	micrurus ni

189	2	6.9	28	1	PETL_CYAPA	P48102	cyanophora
190	2	6.9	28	1	PHR_METTM	P58818	methanobact
191	2	6.9	28	1	PHYB_ASFFI	P81440	aspergillus
192	2	6.9	28	1	PP71_HCMVT	P24429	human cytom
193	2	6.9	28	1	PPOX_BOVIN	P56602	bos taurus
194	2	6.9	28	1	RL5_HALCU	P05972	halobacteri
195	2	6.9	28	1	RS19_PHYS1	O66093	phytoplasma
196	2	6.9	28	1	SCX2_BUTSI	P15230	buthus sind
197	2	6.9	28	1	SLP1_LEIQH	P80669	leiurus qui
198	2	6.9	28	1	SMS2_ORENI	P81029	oreochromis
199	2	6.9	28	1	TXO2_AGEAP	P15971	agelenopsis
200	2	6.9	28	1	VG9_SPV4	P11341	spiroplasma
201	2	6.9	28	1	VIP_DIDMA	P39089	didelphis m
202	2	6.9	28	1	VIP_SCYCA	P09685	scyliorhinu
203	2	6.9	28	1	Y073_ARCFU	O30163	archaeoglob
204	2	6.9	28	1	Y16P_BPT4	P39248	bacterioph
205	2	6.9	28	1	YA79_ARCFU	O29184	archaeoglob
206	2	6.9	29	1	12AH_CLOS4	P21215	clostridium
207	2	6.9	29	1	AL21_HORSE	P81216	equus cabal
208	2	6.9	29	1	ATP9_PICPJ	Q06838	pichia pijp
209	2	6.9	29	1	ATPA_BRYMA	P26965	bryopsis ma
210	2	6.9	29	1	BR2D_RANES	P40840	rana escule
211	2	6.9	29	1	BREE_RANES	P40841	rana escule
212	2	6.9	29	1	CERB_CERCA	P36191	ceratitis c
213	2	6.9	29	1	COA1_BPI22	P15413	bacterioph
214	2	6.9	29	1	COXJ_CANFA	Q9tr29	canis famil
215	2	6.9	29	1	COXK_SHEEP	Q9tr28	ovis aries
216	2	6.9	29	1	CU36_LOCFI	P11737	locusta mig
217	2	6.9	29	1	CXD6_CONGL	Q9twm7	conus glori
218	2	6.9	29	1	CXOC_CONMA	P37300	conus magus
219	2	6.9	29	1	CXOD_CONMA	Q26350	conus magus
220	2	6.9	29	1	CXST_CONGE	P58844	conus geogr
221	2	6.9	29	1	DMS5_PHYSA	P80281	phyllomedus
222	2	6.9	29	1	GLUC_ANAPL	P01276	anas platyr
223	2	6.9	29	1	GLUC_CALMI	P13189	callorhynch
224	2	6.9	29	1	GLUC_DIDMA	P18108	didelphis m
225	2	6.9	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
226	2	6.9	29	1	GLUC_PLAFA	P23062	platichthys
227	2	6.9	29	1	GLUC_RABIT	P25449	oryctolagus
228	2	6.9	29	1	GLUC_TORMA	P09567	torpedo mar
229	2	6.9	29	1	H2B2_ECHES	P13282	echinus esc
230	2	6.9	29	1	HOXY_RHOOP	P22660	rhodococcus
231	2	6.9	29	1	HRJ_BOTJA	P20416	bothrops ja
232	2	6.9	29	1	HS98_NEUCR	P31540	neurospora
233	2	6.9	29	1	ITH3_BOVIN	P56652	bos taurus
234	2	6.9	29	1	ITR1_CUCMA	P01074	cucurbita m
235	2	6.9	29	1	ITR1_LJFCY	P25849	luffa cylin
236	2	6.9	29	1	ITR1_MOMRE	P17680	momordica r
237	2	6.9	29	1	ITR2_BRYDI	P11968	bryonia dio
238	2	6.9	29	1	ITR3_CYCPE	P83394	cyclanthera
239	2	6.9	29	1	ITR4_CYCPE	P83395	cyclanthera
240	2	6.9	29	1	ITR5_CYCPE	P83396	cyclanthera
241	2	6.9	29	1	KDPF_ECOLI	P36937	escherichia
242	2	6.9	29	1	MDH_BURPS	P80536	burkholderi
243	2	6.9	29	1	MULR_ECHML	P81798	echis multi
244	2	6.9	29	1	PETN_ANASP	Q913p6	anabaena sp
245	2	6.9	29	1	PETN_ARATH	P12178	arabidopsis

246	2	6.9	29	1	PETN_CHAGL	Q8ma13 chaetosphae
247	2	6.9	29	1	PETN_CYAPA	P48258 cyanophora
248	2	6.9	29	1	PETN_GUITH	O78498 guillardia
249	2	6.9	29	1	PETN_MAIZE	Q33302 zea mays (m
250	2	6.9	29	1	PETN_MARPO	P12177 marchantia
251	2	6.9	29	1	PETN_MESVI	Q9mus4 mesostigma
252	2	6.9	29	1	PETN_ODOSI	P49527 odontella s
253	2	6.9	29	1	PETN_PINTH	P41611 pinus thunb
254	2	6.9	29	1	PETN_PORPU	P51276 porphyra pu
255	2	6.9	29	1	PETN_PSINU	Q8wi23 psilotum nu
256	2	6.9	29	1	PETN_SKECO	O96807 skeletonema
257	2	6.9	29	1	PETN_SYNEL	Q8dkn2 synechococc
258	2	6.9	29	1	PETN_SYNY3	P72717 synechocyst
259	2	6.9	29	1	PK4_DICDI	P34103 dictyosteli
260	2	6.9	29	1	PRO1_DACGL	P18689 dactylis gl
261	2	6.9	29	1	PSAF_SYNP6	P31083 synechococc
262	2	6.9	29	1	PSAK_SPIOL	P14627 spinacia ol
263	2	6.9	29	1	PSAM_GUITH	O78448 guillardia
264	2	6.9	29	1	PSBI_SYNVC	P12240 synechococc
265	2	6.9	29	1	RL15_HALCU	P05971 halobacteri
266	2	6.9	29	1	RL15_STRLI	P49975 streptomyce
267	2	6.9	29	1	RP54_CLOKL	P38944 clostridium
268	2	6.9	29	1	SCX1_ANDMA	P56215 androctonus
269	2	6.9	29	1	SDHB_CLOPR	P80213 clostridium
270	2	6.9	29	1	SLP2_LEIQH	P80670 leiurus qui
271	2	6.9	29	1	SLP3_LEIQH	P80671 leiurus qui
272	2	6.9	29	1	TAT_HV1Z3	P12510 human immun
273	2	6.9	29	1	TLP_ACTDE	P81370 actinidia d
274	2	6.9	29	1	VARF_VIOAR	P58451 viola arven
275	2	6.9	29	1	Y15_BPT7	P03792 bacterioph
276	2	6.9	29	1	Y51_BPT3	P20326 bacterioph
277	2	6.9	29	1	YCX4_ODOSI	P49830 odontella s
278	2	6.9	29	1	YCX4_ODOSI	P49838 odontella s
279	2	6.9	30	1	2ENR_CLOTY	P11887 clostridium
280	2	6.9	30	1	A1AT_CHIVI	P38026 chinchilla
281	2	6.9	30	1	AATC_RABIT	P12343 oryctolagus
282	2	6.9	30	1	AATM_RABIT	P12345 oryctolagus
283	2	6.9	30	1	ACB1_DIGLA	P81624 digitalis l
284	2	6.9	30	1	AMPT_BACST	P00728 bacillus st
285	2	6.9	30	1	ANF_RANRI	P09196 rana ridibu
286	2	6.9	30	1	CALM_LYTPI	P05935 lytechinus
287	2	6.9	30	1	CBAL_BACST	P13722 bacillus st
288	2	6.9	30	1	CH60_CLOPA	P81339 clostridium
289	2	6.9	30	1	CIRA_CHAPA	P56871 chassalia p
290	2	6.9	30	1	CLPA_PINPS	P81671 pinus pinas
291	2	6.9	30	1	COAE_CORAM	P58101 corynebacte
292	2	6.9	30	1	COXC_SOLTU	P80500 solanum tub
293	2	6.9	30	1	CRG2_SCOWA	P19865 scoliodon w
294	2	6.9	30	1	CX2A_CONBE	P58625 conus betul
295	2	6.9	30	1	CX7A_CONTU	P58923 conus tulip
296	2	6.9	30	1	CXEX_CONCN	P58928 conus conso
297	2	6.9	30	1	CXK4_CONST	P58921 conus stria
298	2	6.9	30	1	CXVB_CONER	P58783 conus ermin
299	2	6.9	30	1	CY35_DESAC	P81079 desulfuromo
300	2	6.9	30	1	CY01_VIOOD	P82230 viola odora
301	2	6.9	30	1	CY08_VIOOD	P58440 viola odora
302	2	6.9	30	1	DEF2_MACMU	P82317 macaca mula

303	2	6.9	30	1	DIDH_COMTE
304	2	6.9	30	1	DIU2_HYLLI
305	2	6.9	30	1	DIU2_MANSE
306	2	6.9	30	1	END2_ONCKE
307	2	6.9	30	1	FIBR_PANIN
308	2	6.9	30	1	GLUM_ANGAN
309	2	6.9	30	1	HCY2_HOMAM
310	2	6.9	30	1	HETA_RADMA
311	2	6.9	30	1	HYPH_HYBPA
312	2	6.9	30	1	IHFB_RHILE
313	2	6.9	30	1	ITI1_LAGLE
314	2	6.9	30	1	ITR1_CITLA
315	2	6.9	30	1	ITR1_MOMCH
316	2	6.9	30	1	ITR2_ECBEL
317	2	6.9	30	1	ITR2_LUFCY
318	2	6.9	30	1	ITR3_CUCMC
319	2	6.9	30	1	ITR3_MOMCO
320	2	6.9	30	1	ITR4_CUCSA
321	2	6.9	30	1	ITR6_CYCPE
322	2	6.9	30	1	ITR7_CYCPE
323	2	6.9	30	1	KAB5_OLDAF
324	2	6.9	30	1	LAS1_PIG
325	2	6.9	30	1	LEAH_PHAVU
326	2	6.9	30	1	MDH_HELGE
327	2	6.9	30	1	MMAL_DERMI
328	2	6.9	30	1	NU5M_PISOC
329	2	6.9	30	1	NUO2_SOLTU
330	2	6.9	30	1	P2CO_ARTSP
331	2	6.9	30	1	PCCA_MYXXA
332	2	6.9	30	1	PCG1_PACGO
333	2	6.9	30	1	PCG5_PACGO
334	2	6.9	30	1	PETN_NEPOL
335	2	6.9	30	1	PLF4_RABIT
336	2	6.9	30	1	PLMS_SQUAC
337	2	6.9	30	1	PMGY_CANAL
338	2	6.9	30	1	PRT1_CLUPA
339	2	6.9	30	1	PRT2_ONCMY
340	2	6.9	30	1	PRT3_ONCMY
341	2	6.9	30	1	PRT4_ONCMY
342	2	6.9	30	1	PRTB_ONCMY
343	2	6.9	30	1	PSAM_CYACA
344	2	6.9	30	1	PSAM_MESVI
345	2	6.9	30	1	PSAM_ODOSI
346	2	6.9	30	1	PSAM_PINTH
347	2	6.9	30	1	PYSD_METBA
348	2	6.9	30	1	RIPS_MOMCO
349	2	6.9	30	1	RKGG_LEPKE
350	2	6.9	30	1	RNP_ODOVI
351	2	6.9	30	1	SCK2_TITSE
352	2	6.9	30	1	SCX2_CENLI
353	2	6.9	30	1	SILU_RHIPU
354	2	6.9	30	1	TAT_HV1ZH
355	2	6.9	30	1	TL1X_SPIOL
356	2	6.9	30	1	TL29_SPIOL
357	2	6.9	30	1	TX2_HETVE
358	2	6.9	30	1	UC35_MAIZE
359	2	6.9	30	1	UDDP_SULAC

P80702	comamonas t
P82015	hyles linea
P24858	manduca sex
P01205	oncorhynchu
P22775	panulirus i
P41521	anguilla an
P82297	homarus ame
P58691	radianthus
P58445	hybanthus p
P80606	rhizobium l
P26771	lagenaria l
P11969	citrullus l
P10294	momordica c
P12071	ecballium e
P25850	luffa cylin
P32041	cucumis mel
P82410	momordica c
P10292	cucumis sat
P83397	cyclanthera
P83398	cyclanthera
P58456	oldenlandia
P80171	sus scrofa
P81870	phaseolus v
P80037	heliobacter
P16312	dermatophag
P24999	pisaster oc
P80268	solanum tub
P37365	arthrobacte
P81185	myxococcus
P82414	pachycondyl
P82418	pachycondyl
Q9t101	nephroselmi
P83470	oryctolagus
P82542	squalus aca
P82612	candida alb
P02335	clupea pall
P02331	oncorhynchu
P02332	oncorhynchu
P02333	oncorhynchu
P12819	oncorhynchu
Q9tlx5	cyanidium c
Q9mus2	mesostigma
P49487	odontella s
P41601	pinus thunb
P80524	methanosarc
P20655	momordica c
P21587	lepidochely
P19640	odocoileus
P08816	tityus serr
P18927	centruroide
P02885	rhizomucor
P12512	human immun
P82537	spinacia ol
P81833	spinacia ol
P58426	heteropoda
P80641	zea mays (m
P80143	sulfolobus

360	2	6.9	30	1	URE1_ECOLI
361	2	6.9	30	1	VAA1_EQUAR
362	2	6.9	30	1	VAA1_PSINU
363	2	6.9	30	1	VAA2_PSINU
364	2	6.9	30	1	VATN_BOVIN
365	2	6.9	30	1	VG03_BPPF1
366	2	6.9	30	1	VPU_HV1SC
367	2	6.9	30	1	VTTA_BPT3
368	2	6.9	30	1	Y161_TREPA
369	2	6.9	30	1	Y357_BORBU
370	2	6.9	30	1	Y425_BORBU
371	2	6.9	30	1	Y573_TREPA
372	2	6.9	30	1	Y932_TREPA
373	2	6.9	30	1	YCCB_ECOLI
374	2	6.9	31	1	A98A_DROME
375	2	6.9	31	1	BCAM_PIG
376	2	6.9	31	1	CIRB_CHAPA
377	2	6.9	31	1	COG5_BOVIN
378	2	6.9	31	1	COX4_NEUCR
379	2	6.9	31	1	CTRP_PENMO
380	2	6.9	31	1	CU54_LOCFI
381	2	6.9	31	1	CXD6_CONNI
382	2	6.9	31	1	CXG6_CONTE
383	2	6.9	31	1	CYLA_PSYLO
384	2	6.9	31	1	DEF2_MESAU
385	2	6.9	31	1	EFTU_STRLU
386	2	6.9	31	1	ENDB_CAMDR
387	2	6.9	31	1	ER29_BOVIN
388	2	6.9	31	1	ETFD_PARDE
389	2	6.9	31	1	FIBB_CANFA
390	2	6.9	31	1	GT_SERMA
391	2	6.9	31	1	HBA_MACEU
392	2	6.9	31	1	HCY1_HOMAM
393	2	6.9	31	1	HCY2_MAISQ
394	2	6.9	31	1	HEM2_PHAGO
395	2	6.9	31	1	LC70_LACPA
396	2	6.9	31	1	LCCB_LEUME
397	2	6.9	31	1	LPRM_ECOLI
398	2	6.9	31	1	MDH_STRAR
399	2	6.9	31	1	NAP4_HUMAN
400	2	6.9	31	1	PETL_ANASP
401	2	6.9	31	1	PETL_ARATH
402	2	6.9	31	1	PETL_BETVU
403	2	6.9	31	1	PETL_CHLVU
404	2	6.9	31	1	PETL_GUIITH
405	2	6.9	31	1	PETL_MAIZE
406	2	6.9	31	1	PETL_ODOSI
407	2	6.9	31	1	PETL_OENHO
408	2	6.9	31	1	PETL_ORYSA
409	2	6.9	31	1	PETL_PORPU
410	2	6.9	31	1	PETL_PSINU
411	2	6.9	31	1	PETL_SPIOL
412	2	6.9	31	1	PETL_WHEAT
413	2	6.9	31	1	PETM_CYACA
414	2	6.9	31	1	PETN_CYACA
415	2	6.9	31	1	PRT2_CLUPA
416	2	6.9	31	1	PSAK_ANAVA

Q03284	escherichia
Q04236	equisetum a
Q04237	psilotum nu
Q04239	psilotum nu
P81134	bos taurus
P25137	bacterioph
P05948	human immun
P20837	bacterioph
O83196	treponema p
O51332	borrelia bu
O51386	borrelia bu
O83583	treponema p
O83902	treponema p
P24244	escherichia
O46201	drosophila
O19098	sus scrofa
P56879	chassalia p
P83437	bos taurus
P06809	neurospora
P35002	penaeus mon
P11738	locusta mig
P56710	conus nigro
P58922	conus texti
P56872	psychotria
P81466	mesocricetu
P52390	streptomyce
P01203	camelus dro
P81623	bos taurus
P55932	paracoccus
P02677	canis famil
P22416	serratia ma
P81043	macropus eu
P82296	homarus ame
P82303	maia squina
P27687	phascolopsi
P80959	lactobacill
P81052	leuconostoc
P10739	escherichia
P19982	streptomyce
P19877	homo sapien
Q8yvq2	anabaena sp
P56776	arabidopsis
P46612	beta vulgar
P56306	chlorella v
O78468	guillardia
P19445	zea mays (m
P49524	odontella s
Q9mtk4	oenothera h
P12180	oryza sativ
P51221	porphyra pu
Q8wi03	psilotum nu
Q9m310	spinacia ol
P58247	triticum ae
Q9t1r5	cyanidium c
Q9t1r6	cyanidium c
P02336	clupea pall
P23317	anabaena va

417	2	6.9	31	1	PSAM_CHLVU	P56314	chlorella v
418	2	6.9	31	1	PSAM_CYAPA	P48185	cyanophora
419	2	6.9	31	1	PSBK_SYNVU	P19054	synechococc
420	2	6.9	31	1	PSBM_MESVI	Q9muq7	mesostigma
421	2	6.9	31	1	PSBT_CHLRE	P37256	chlamydomon
422	2	6.9	31	1	PSBT_CHLVU	P56327	chlorella v
423	2	6.9	31	1	PSBT_CYAPA	P48109	cyanophora
424	2	6.9	31	1	PSBT_EUGGR	P20176	euglena gra
425	2	6.9	31	1	PSBT_MESVI	Q9muv6	mesostigma
426	2	6.9	31	1	PSBT_PORPU	P51323	porphyra pu
427	2	6.9	31	1	PYSG_METBA	P80523	methanosarc
428	2	6.9	31	1	RECX_METCL	P37865	methylomona
429	2	6.9	31	1	RL21_STRTR	P48956	streptococc
430	2	6.9	31	1	SARL_HUMAN	O00631	homo sapien
431	2	6.9	31	1	SC37_MESMA	P83407	mesobuthus
432	2	6.9	31	1	SODC_STRHE	P81163	striga herm
433	2	6.9	31	1	TX3_HETVE	P58427	heteropoda
434	2	6.9	31	1	TXA3_PARAC	P09949	parasicyoni
435	2	6.9	31	1	Y191_BORBU	O51209	borrelia bu
436	2	6.9	31	1	Y3KD_BPCHP	P19187	bacteriopha
437	2	6.9	31	1	Y603_ARCFU	O29652	archaeoglob
438	2	6.9	32	1	A2M_PACLE	P20738	pacifastacu
439	2	6.9	32	1	APL3_DIAGR	P81471	diatraea gr
440	2	6.9	32	1	ATP0_PIG	P80021	sus scrofa
441	2	6.9	32	1	ATP7_SPIOL	P80088	spinacia ol
442	2	6.9	32	1	ATPO_SPIOL	P80087	spinacia ol
443	2	6.9	32	1	B4G1_RAT	P80225	r beta-1,4-
444	2	6.9	32	1	CAAP_MICEC	P21162	micromonosp
445	2	6.9	32	1	CAL0_BOVIN	P01260	bos taurus
446	2	6.9	32	1	CAL0_PIG	P01259	sus scrofa
447	2	6.9	32	1	CAR1_ECHCA	Q9prp9	echis carin
448	2	6.9	32	1	CEC_OIKKI	P83420	oiketicus k
449	2	6.9	32	1	COA1_BPIF1	O80295	bacteriopha
450	2	6.9	32	1	COA1_BPIKE	P03676	bacteriopha
451	2	6.9	32	1	COA2_BPFD	P03677	bacteriopha
452	2	6.9	32	1	CRP_PLEPL	P12245	pleuronecte
453	2	6.9	32	1	CXG7_CONPE	P56711	conus penna
454	2	6.9	32	1	CYBL_RHOGR	P32953	rhodotorula
455	2	6.9	32	1	CYSB_FASHE	P80529	fasciola he
456	2	6.9	32	1	DBH_SYNY1	P02343	synechocyst
457	2	6.9	32	1	ER29_CHICK	P81628	gallus gall
458	2	6.9	32	1	ER29_TRIVU	P81629	trichosurus
459	2	6.9	32	1	ERH_PIG	P80230	sus scrofa
460	2	6.9	32	1	FER_PORCR	P18821	porphyridiu
461	2	6.9	32	1	FLA1_METHU	P17603	methanospir
462	2	6.9	32	1	FRIH_ANAPL	P80145	anas platyr
463	2	6.9	32	1	GHR4_RAT	P33581	rattus norv
464	2	6.9	32	1	GLB4_LAMSP	P20413	lamellibrac
465	2	6.9	32	1	GT82_DICLA	P82608	dicentrarch
466	2	6.9	32	1	H2AZ_ONCMY	P22647	oncorhynchu
467	2	6.9	32	1	HCYC_CHEDE	P83172	cherax dest
468	2	6.9	32	1	IAPP_BOVIN	Q28207	bos taurus
469	2	6.9	32	1	IAPP_SAGOE	Q28934	saguinus oe
470	2	6.9	32	1	IAPP_SHEEP	Q28605	ovis aries
471	2	6.9	32	1	ILVB_ENTAE	Q09129	enterobacte
472	2	6.9	32	1	ITR2_CUCSA	P10291	cucumis sat
473	2	6.9	32	1	LPID_ECOLI	P03060	escherichia

474	2	6.9	32	1	LPID_EDWTA	P08140	edwardsiell
475	2	6.9	32	1	LPIV_ECOLI	P03061	escherichia
476	2	6.9	32	1	MDH_NITAL	P10887	nitzschia a
477	2	6.9	32	1	NEUB_PIG	P01297	sus scrofa
478	2	6.9	32	1	OVOS_ANAPL	P20739	anas platyr
479	2	6.9	32	1	PA22_AGKHP	P18997	agkistrodon
480	2	6.9	32	1	PA2_RHONO	P43318	rhophilema n
481	2	6.9	32	1	PETL_CHLRE	P50369	chlamydomon
482	2	6.9	32	1	PETM_PORPU	P51275	porphyra pu
483	2	6.9	32	1	PHNS_DESMU	P13062	desulfovibr
484	2	6.9	32	1	PRI3_ONCMY	P02330	oncorhynchu
485	2	6.9	32	1	PRT1_ONCKE	P02327	oncorhynchu
486	2	6.9	32	1	PRT4_SCYCA	P30259	scyliorhinu
487	2	6.9	32	1	PRT5_ONCMY	P02334	oncorhynchu
488	2	6.9	32	1	PRT6_ONCMY	P08145	oncorhynchu
489	2	6.9	32	1	PRT7_ONCMY	P08146	oncorhynchu
490	2	6.9	32	1	PRT8_ONCMY	P12817	oncorhynchu
491	2	6.9	32	1	PRT9_ONCMY	P08147	oncorhynchu
492	2	6.9	32	1	PRTA_ONCMY	P12818	oncorhynchu
493	2	6.9	32	1	PRT_ORYLA	Q91185	oryzias lat
494	2	6.9	32	1	PSBT_CYACA	O19927	cyanidium c
495	2	6.9	32	1	PSBT_GUITH	O78512	guillardia
496	2	6.9	32	1	PSBZ_EUGAN	Q8s195	euglena ana
497	2	6.9	32	1	PSBZ_EUGMY	Q8s191	euglena myx
498	2	6.9	32	1	RIP2_PHYDI	P34967	phytolacca
499	2	6.9	32	1	RK1_RABIT	P81655	oryctolagus
500	2	6.9	32	1	RS19_YEREN	Q56847	yersinia en
501	2	6.9	32	1	SCK2_CENNO	P58504	centruroide
502	2	6.9	32	1	TAT_SIVM2	P05912	simian immu
503	2	6.9	32	1	TRYP_PENMO	P35050	penaeus mon
504	2	6.9	32	1	TX29_PHONI	P29426	phoneutria
505	2	6.9	32	1	TXP7_APTSC	P49271	aptostichus
506	2	6.9	32	1	UC09_MAIZE	P80615	zea mays (m
507	2	6.9	32	1	Y169_TREPA	O83199	treponema p
508	2	6.9	32	1	Y433_BORBU	O51394	borrelia bu
509	2	6.9	32	1	YH17_HAEIN	P44295	haemophilus
510	2	6.9	32	1	YSCA_YEREN	Q01242	yersinia en
511	2	6.9	32	1	YTK3_ILTVT	P23985	infectious
512	2	6.9	33	1	ACT_DICVI	Q24733	dictyocaulu
513	2	6.9	33	1	ALOX_PICPA	P04842	pichia past
514	2	6.9	33	1	ANP3_MYOSC	P04367	myoxocephal
515	2	6.9	33	1	ANP5_MYOAE	P20421	myoxocephal
516	2	6.9	33	1	ATP7_SOLTU	P80496	solanum tub
517	2	6.9	33	1	BR2A_RANES	P40837	rana escule
518	2	6.9	33	1	BR2B_RANES	P40838	rana escule
519	2	6.9	33	1	BR2E_RANES	P32413	rana escule
520	2	6.9	33	1	BR2_RANBP	P32424	rana brevip
521	2	6.9	33	1	CECB_HELVI	P83414	heliiothis v
522	2	6.9	33	1	CECC_HELVI	P83415	heliiothis v
523	2	6.9	33	1	COA1_BPFD	P03675	bacteriopha
524	2	6.9	33	1	COA2_BPI22	P15414	bacteriopha
525	2	6.9	33	1	COA2_BPIKE	P03678	bacteriopha
526	2	6.9	33	1	COXL_ONCMY	P80330	oncorhynchu
527	2	6.9	33	1	CU89_HUMAN	P59042	homo sapien
528	2	6.9	33	1	CXBW_CONRA	P58804	conus radia
529	2	6.9	33	1	CXO_CONVE	P83301	conus ventr
530	2	6.9	33	1	DBB2_DOLAU	P83376	dolabella a

531	2	6.9	33	1	DEF1_MESAU	P81465	mesocricetu
532	2	6.9	33	1	DEF3_MESAU	P81467	mesocricetu
533	2	6.9	33	1	DEF4_MESAU	P81468	mesocricetu
534	2	6.9	33	1	DHE3_PIG	P42174	sus scrofa
535	2	6.9	33	1	FER_PORAE	P18820	porphyridiu
536	2	6.9	33	1	GAST_CAVPO	P06885	cavia porce
537	2	6.9	33	1	GAST_CHIBR	P10034	chinchilla
538	2	6.9	33	1	GAST_DIDMA	P33713	didelphis m
539	2	6.9	33	1	GGN2_RANRU	P80396	rana rugosa
540	2	6.9	33	1	GGN3_RANRU	P80397	rana rugosa
541	2	6.9	33	1	GLU2_ORENI	P81027	oreochromis
542	2	6.9	33	1	HF40_MAIZE	P82865	zea mays (m
543	2	6.9	33	1	HOXU_RHOOP	P22659	rhodococcus
544	2	6.9	33	1	LPPY_SALTY	P08522	salmonella
545	2	6.9	33	1	LPRH_ECOLI	P37324	escherichia
546	2	6.9	33	1	LYC2_HORSE	P81710	equus cabal
547	2	6.9	33	1	MBP1_MAIZE	P28794	zea mays (m
548	2	6.9	33	1	MHAA_STRCH	P80435	streptomyce
549	2	6.9	33	1	MYMY_MYTED	P81614	mytilus edu
550	2	6.9	33	1	OTCC_PSEPU	P11727	pseudomonas
551	2	6.9	33	1	PEN3_ADECU	P35987	canine aden
552	2	6.9	33	1	PETM_CYAPA	P48366	cyanophora
553	2	6.9	33	1	PETM_SYNEL	Q8dj15	synechococc
554	2	6.9	33	1	PK1_DICDI	P34101	dictyosteli
555	2	6.9	33	1	PK5_DICDI	P34104	dictyosteli
556	2	6.9	33	1	PRI1_ONCMY	P02326	oncorhynchu
557	2	6.9	33	1	PRI2_ONCMY	P02328	oncorhynchu
558	2	6.9	33	1	PRTB_MUGCE	P08130	mugil cepha
559	2	6.9	33	1	PRTL_ECOLI	P02338	escherichia
560	2	6.9	33	1	PSAK_CUCSA	P42051	cucumis sat
561	2	6.9	33	1	PSBT_ARATH	P37259	arabidopsis
562	2	6.9	33	1	PSBT_MAIZE	P37257	zea mays (m
563	2	6.9	33	1	RL21_XENLA	P49628	xenopus lae
564	2	6.9	33	1	RL26_XENLA	P49629	xenopus lae
565	2	6.9	33	1	RL28_XENLA	P46780	xenopus lae
566	2	6.9	33	1	RL4_HALCU	P05967	halobacteri
567	2	6.9	33	1	RPOC_HETCA	P36441	heterosigma
568	2	6.9	33	1	RRPO_BPBZ1	P09674	bacteriopha
569	2	6.9	33	1	RS4_XENLA	P49401	xenopus lae
570	2	6.9	33	1	RT25_BOVIN	P82669	bos taurus
571	2	6.9	33	1	RUGA_RANRU	P80954	rana rugosa
572	2	6.9	33	1	SCX9_BUTOC	P04099	buthus occi
573	2	6.9	33	1	THIO_CLOST	P81109	clostridium
574	2	6.9	33	1	TX1_HETVE	P58425	heteropoda
575	2	6.9	33	1	TXH1_SELHU	P56676	selenocosmi
576	2	6.9	33	1	TXN3_SELHA	P83464	selenocosmi
577	2	6.9	33	1	VT1B_RAT	P58200	rattus norv
578	2	6.9	33	1	Y474_BORBU	O51430	borrelia bu
579	2	6.9	33	1	Y656_TREPA	O83662	treponema p
580	2	6.9	33	1	Y849_BORBU	O51789	borrelia bu
581	2	6.9	33	1	YC12_CHLRE	P50370	chlamydomon
582	2	6.9	33	1	YC12_MARPO	P31560	marchantia
583	2	6.9	33	1	YC12_MESVI	Q9mus3	mesostigma
584	2	6.9	33	1	YC12_NEPOL	Q9tky6	nephroselmi
585	2	6.9	33	1	YC12_PINTH	P41600	pinus thunb
586	2	6.9	33	1	YL74_ARCFU	O28108	archaeoglob
587	2	6.9	33	1	YLCH_BP82	Q37869	bacteriopha

588	2	6.9	33	1	YLCH_ECOLI	Q47268	escherichia
589	2	6.9	34	1	AMP2_CHICK	P80390	gallus gall
590	2	6.9	34	1	ASPG_PIG	P30918	sus scrofa
591	2	6.9	34	1	BR2C_RANES	P40839	rana escule
592	2	6.9	34	1	COL_CHICK	P11148	gallus gall
593	2	6.9	34	1	COXA_THETH	P82543	thermus the
594	2	6.9	34	1	COXG_THUOB	P80976	thunnus obe
595	2	6.9	34	1	CXGS_CONGE	P15472	conus geogr
596	2	6.9	34	1	DEF2_RABIT	P07468	oryctolagus
597	2	6.9	34	1	DEF7_RABIT	P80223	oryctolagus
598	2	6.9	34	1	ECAB_ECTTU	P49344	ectatomma t
599	2	6.9	34	1	EF2_RABIT	P55823	oryctolagus
600	2	6.9	34	1	EGGR_APLCA	P01363	aplysia cal
601	2	6.9	34	1	GAST_CAPHI	P04564	capra hircu
602	2	6.9	34	1	H1S_STRPU	P19376	strongyloce
603	2	6.9	34	1	HS7S_CUCMA	P31082	cucurbita m
604	2	6.9	34	1	ITR1_MOMCO	P82408	momordica c
605	2	6.9	34	1	ITR2_MOMCO	P82409	momordica c
606	2	6.9	34	1	LPTN_PROVU	P28779	proteus vul
607	2	6.9	34	1	M44E_HUMAN	Q96pgl	homo sapien
608	2	6.9	34	1	MYTB_MYTED	P81613	mytilus edu
609	2	6.9	34	1	PETM_ANASP	Q9f4w2	anabaena sp
610	2	6.9	34	1	PRT1_SAROR	P25327	sarda orien
611	2	6.9	34	1	PRT1_SCOSC	P83264	scomber sco
612	2	6.9	34	1	PRT1_THUTH	P02321	thunnus thy
613	2	6.9	34	1	PRT2_SCOSC	P83265	scomber sco
614	2	6.9	34	1	PRT2_THUTH	P02322	thunnus thy
615	2	6.9	34	1	PRT_DICLA	Q9ps27	dicentrarch
616	2	6.9	34	1	PRT_PERFV	P29629	perca flave
617	2	6.9	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
618	2	6.9	34	1	PSAI_OENHO	Q9mtl2	oenothera h
619	2	6.9	34	1	PSBM_ARATH	P12169	arabidopsis
620	2	6.9	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
621	2	6.9	34	1	PSBM_CHLRE	P92277	chlamydomon
622	2	6.9	34	1	PSBM_MAIZE	P48189	zea mays (m
623	2	6.9	34	1	PSBM_MARPO	P12168	marchantia
624	2	6.9	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
625	2	6.9	34	1	PSBM_OENHO	Q9mtm8	oenothera h
626	2	6.9	34	1	PSBM_PEA	P34833	pisum sativ
627	2	6.9	34	1	PSBM_PSINU	Q8wi22	psilotum nu
628	2	6.9	34	1	PSBM_WHEAT	Q9xps6	triticum ae
629	2	6.9	34	1	PSBT_TOBAC	P12184	nicotiana t
630	2	6.9	34	1	PSPC_BOVIN	P15783	bos taurus
631	2	6.9	34	1	PSPC_CANFA	P22397	canis famil
632	2	6.9	34	1	PYSB_METBA	P80522	methanosarc
633	2	6.9	34	1	RNLI_PIG	P15466	sus scrofa
634	2	6.9	34	1	RR2_OCHNE	Q40606	ochrosphaer
635	2	6.9	34	1	SCXM_SCOMA	P80719	scorpio mau
636	2	6.9	34	1	SMS_MYXGL	P19209	myxine glut
637	2	6.9	34	1	THEM_MALSU	P13858	malbranchea
638	2	6.9	34	1	TX33_PHONI	P81789	phoneutria
639	2	6.9	34	1	TXP5_BRASM	P49266	brachypelma
640	2	6.9	34	1	VLYS_BPM1	P08229	bacterioph
641	2	6.9	34	1	VPU_HV1W2	P08808	human immun
642	2	6.9	34	1	Y05J_BPT4	P39239	bacterioph
643	2	6.9	34	1	Y224_TREPA	O83253	treponema p
644	2	6.9	34	1	Y848_BORBU	O51788	borrelia bu

645	2	6.9	34	1	Y870_HAEIN	P44065	haemophilus
646	2	6.9	34	1	Y967_HAEIN	P44086	haemophilus
647	2	6.9	34	1	YC12_GUITH	O78460	guillardia
648	2	6.9	34	1	YC12_ODOSI	P49529	odontella s
649	2	6.9	34	1	YC12_PORPU	P51385	porphyra pu
650	2	6.9	34	1	YC12_SKECO	O96797	skeletonema
651	2	6.9	34	1	YMIA_AGRTU	P38437	agrobacteri
652	2	6.9	34	1	Z33B_HUMAN	Q06731	homo sapien
653	2	6.9	35	1	ADO1_AGRDO	P58608	agriosphodr
654	2	6.9	35	1	C550_BACHA	P80091	bacillus ha
655	2	6.9	35	1	CEC4_BOMMO	P14666	bombyx mori
656	2	6.9	35	1	CECA_HELVI	P83413	heliopsis v
657	2	6.9	35	1	CECB_ANTPE	P01509	antheraea p
658	2	6.9	35	1	D3HI_RABIT	P32185	oryctolagus
659	2	6.9	35	1	DEFB_MYTED	P81611	mytilus edu
660	2	6.9	35	1	END4_YEREN	P42691	yersinia en
661	2	6.9	35	1	ERFK_KLEAE	Q08599	klebsiella
662	2	6.9	35	1	EXE2_HELVS	P04204	heloderma s
663	2	6.9	35	1	FAS_CAPHI	P08757	capra hircu
664	2	6.9	35	1	FLAV_NOSSM	P35707	nostoc sp.
665	2	6.9	35	1	GBGU_MOUSE	Q61017	mus musculu
666	2	6.9	35	1	GRDB_CLOPU	P55793	clostridium
667	2	6.9	35	1	GUR_GYMSY	P25810	gymnema syl
668	2	6.9	35	1	HMWC_DESGI	P38588	desulfovibr
669	2	6.9	35	1	IAAC_HORVU	P34951	hordeum vul
670	2	6.9	35	1	KPPR_PINPS	P81664	pinus pinas
671	2	6.9	35	1	LCGB_LACLA	P36962	lactococcus
672	2	6.9	35	1	NEF_HV1H3	P05854	human immun
673	2	6.9	35	1	PBP1_LYMDI	P34176	lymantria d
674	2	6.9	35	1	PBP2_LYMDI	P34177	lymantria d
675	2	6.9	35	1	PBP_HYACE	P34175	hyalophora
676	2	6.9	35	1	PBP_ORGPS	P34178	orgyia pseu
677	2	6.9	35	1	PHI1_MYTCA	P35422	mytilus cal
678	2	6.9	35	1	PSAI_CYAPA	P48116	cyanophora
679	2	6.9	35	1	PSBT_MARPO	P12182	marchantia
680	2	6.9	35	1	PSBT_OENHO	P37258	oenothera h
681	2	6.9	35	1	PSBT_ORYSA	P12183	oryza sativ
682	2	6.9	35	1	PSBT_PINTH	P41625	pinus thunb
683	2	6.9	35	1	PSPC_PIG	P15785	sus scrofa
684	2	6.9	35	1	RL32_HALCU	P05965	halobacteri
685	2	6.9	35	1	SCKB_PANIM	P55928	pandinus im
686	2	6.9	35	1	SCKG_PANIM	Q10726	pandinus im
687	2	6.9	35	1	SCX1_BUTSI	P15229	buthus sind
688	2	6.9	35	1	SCX5_BUTEU	P15222	buthus eupe
689	2	6.9	35	1	SCXP_ANDMA	P01498	androctonus
690	2	6.9	35	1	SMS_LAMFL	Q9prro	lampetra fl
691	2	6.9	35	1	SPRC_PIG	P20112	sus scrofa
692	2	6.9	35	1	THPA_THADA	P21381	thaumatococ
693	2	6.9	35	1	TMTX_MESTA	Q9bn12	mesobuthus
694	2	6.9	35	1	TXAG_AGEOP	P31328	agelena opu
695	2	6.9	35	1	TXH4_SELHU	P83303	selenocosmi
696	2	6.9	35	1	TXKS_STOHE	P29187	stoichactis
697	2	6.9	35	1	TXN4_SELHA	P83471	selenocosmi
698	2	6.9	35	1	VL3_PAPVD	P06919	deer papill
699	2	6.9	35	1	VSPA_CERVI	P18692	cerastes vi
700	2	6.9	35	1	WSP7_PINPS	P81086	pinus pinas
701	2	6.9	35	1	Y210_HAEIN	P43964	haemophilus

702	2	6.9	35	1	Y320_BORBU	051299	borrelia bu
703	2	6.9	35	1	Y37_BPT3	P20325	bacteriopha
704	2	6.9	35	1	Y644_ARCFU	O29613	archaeoglob
705	2	6.9	35	1	Y845_BORBU	O51785	borrelia bu
706	2	6.9	35	1	Y847_BORBU	O51787	borrelia bu
707	2	6.9	35	1	YC12_CYACA	Q9tlx0	cyanidium c
708	2	6.9	35	1	YC69_ARCFU	O28999	archaeoglob
709	2	6.9	35	1	YQB5_CAEEL	Q09258	caenorhabdi
710	2	6.9	36	1	AMPL_PIG	P28839	sus scrofa
711	2	6.9	36	1	ANFV_ANGJA	P22642	anguilla ja
712	2	6.9	36	1	C3L1_BOVIN	P30922	bos taurus
713	2	6.9	36	1	CBBA_NITVU	P37102	nitrobacter
714	2	6.9	36	1	CECD_ANTPE	P01511	antheraea p
715	2	6.9	36	1	CYC7_GEOME	P81894	geobacter m
716	2	6.9	36	1	F4RE_METOG	P80951	methanogeni
717	2	6.9	36	1	GLU1_ORENI	P81026	oreochromis
718	2	6.9	36	1	GLUC_HYDCO	P09682	hydrolagus
719	2	6.9	36	1	H1L5_ENSMI	P27203	ensis minor
720	2	6.9	36	1	HBB_PONPY	Q9tt34	pongo pygma
721	2	6.9	36	1	IAA_STRAU	P04082	streptomyce
722	2	6.9	36	1	IOB1_ISYOB	P58609	isyndus obs
723	2	6.9	36	1	KAD_STRGR	P53398	streptomyce
724	2	6.9	36	1	LHG_RHOVI	P04126	rhodopseudo
725	2	6.9	36	1	LYOX_PIG	P45845	sus scrofa
726	2	6.9	36	1	MFA1_YEAST	P34165	saccharomyc
727	2	6.9	36	1	MPG2_DACGL	Q41183	dactylis gl
728	2	6.9	36	1	MYPC_RAT	P56741	rattus norv
729	2	6.9	36	1	NEUH_CARCA	P11975	cardisoma c
730	2	6.9	36	1	NEUY_GADMO	P80167	gadus morhu
731	2	6.9	36	1	NEUY_ONCMY	P29071	oncorhynch
732	2	6.9	36	1	NEUY_RABIT	P09640	oryctolagus
733	2	6.9	36	1	NEUY_RANRI	P29949	rana ridibu
734	2	6.9	36	1	NIFH_ENTAG	P26249	enterobacte
735	2	6.9	36	1	NLTP_PINPI	P26912	pinus pinea
736	2	6.9	36	1	NUCM_SOLTU	P80264	solanum tub
737	2	6.9	36	1	OST2_CHICK	P80897	gallus gall
738	2	6.9	36	1	PAHO_ALLMI	P06305	alligator m
739	2	6.9	36	1	PAHO_ANSAN	P06304	anser anser
740	2	6.9	36	1	PAHO_CERSI	P37999	ceratotheri
741	2	6.9	36	1	PAHO_DIDMA	P18107	didelphis m
742	2	6.9	36	1	PAHO_EQUZE	P38000	equus zebra
743	2	6.9	36	1	PAHO_ERIEU	P41335	erinaceus e
744	2	6.9	36	1	PAHO_LARAR	P41337	larus argen
745	2	6.9	36	1	PAHO_MACMU	P33684	macaca mula
746	2	6.9	36	1	PAHO_RABIT	P41336	oryctolagus
747	2	6.9	36	1	PAHO_RANCA	P15427	rana catesb
748	2	6.9	36	1	PAHO_RANTE	P31229	rana tempor
749	2	6.9	36	1	PAHO_STRCA	P11967	struthio ca
750	2	6.9	36	1	PAHO_TAPPI	P39659	tapirus pin
751	2	6.9	36	1	PGKH_CHLFU	P36232	chlorella f
752	2	6.9	36	1	PMY_PETMA	P80024	petromyzon
753	2	6.9	36	1	PSAH_PEA	P20121	pisum sativ
754	2	6.9	36	1	PSAI_ANGLY	P28251	angiopteris
755	2	6.9	36	1	PSAI_BRAOL	Q31909	brassica ol
756	2	6.9	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
757	2	6.9	36	1	PSAI_CHLVU	P58214	chlorella v
758	2	6.9	36	1	PSAI_CYACA	Q9tm24	cyanidium c

759	2	6.9	36	1	PSAI_HORVU	P13165	hordeum vul
760	2	6.9	36	1	PSAI_MAIZE	P30980	zea mays (m
761	2	6.9	36	1	PSAI_MARPO	P12185	marchantia
762	2	6.9	36	1	PSAI_MESVI	Q9muq4	mesostigma
763	2	6.9	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
764	2	6.9	36	1	PSAI_ORYSA	P12186	oryza sativ
765	2	6.9	36	1	PSAI_PICAB	O47040	picea abies
766	2	6.9	36	1	PSAI_PORPU	P51387	porphyra pu
767	2	6.9	36	1	PSAI_PSINU	Q8wi10	psilotum nu
768	2	6.9	36	1	PSAI_SKECO	O96813	skeletonema
769	2	6.9	36	1	PSAI_TOBAC	P12187	nicotiana t
770	2	6.9	36	1	PSAI_WHEAT	P25410	triticum ae
771	2	6.9	36	1	PSBI_ARATH	P09970	arabidopsis
772	2	6.9	36	1	PSBI_HORVU	P25876	hordeum vul
773	2	6.9	36	1	PSBI_MARPO	P09969	marchantia
774	2	6.9	36	1	PSBI_ORYSA	P12161	oryza sativ
775	2	6.9	36	1	PSBI_PINTH	P41599	pinus thunb
776	2	6.9	36	1	PSBI_PSEMZ	P29796	pseudotsuga
777	2	6.9	36	1	PSBM_CHLVU	P56325	chlorella v
778	2	6.9	36	1	PSBM_SYNEL	Q8dha7	synechococc
779	2	6.9	36	1	PSBY_ODOSI	P49543	odontella s
780	2	6.9	36	1	PSBY_PORPU	P51206	porphyra pu
781	2	6.9	36	1	PYY_AMICA	P29205	amia calva
782	2	6.9	36	1	PYY_LEPSP	P09473	lepisosteus
783	2	6.9	36	1	PYY_MYOSC	P09641	myoxocephal
784	2	6.9	36	1	PYY_ONCKI	P09474	oncorhynchu
785	2	6.9	36	1	PYY_ORENI	P81028	oreochromis
786	2	6.9	36	1	PYY_PIG	P01305	sus scrofa
787	2	6.9	36	1	PYY_RAJRH	P29206	raja rhina
788	2	6.9	36	1	PYY_RANRI	P29204	rana ridibu
789	2	6.9	36	1	SCK2_CENLL	P45630	centruroide
790	2	6.9	36	1	SCK3_LEIQH	P45660	leiurus qui
791	2	6.9	36	1	SCX1_BUTEU	P15220	buthus eupe
792	2	6.9	36	1	SCXL_LEIQU	P45639	leiurus qui
793	2	6.9	36	1	SPYY_PHYBI	P80952	phyllomedus
794	2	6.9	36	1	TAEK_ACTEQ	P81897	actinia equ
795	2	6.9	36	1	TLN1_CHICK	P54939	gallus gall
796	2	6.9	36	1	TX1B_AGEAP	P15970	agelenopsis
797	2	6.9	36	1	TXAM_METSE	P11495	metridium s
798	2	6.9	36	1	TXD3_PARLU	P83258	paracaelote
799	2	6.9	36	1	TXJB_HADVE	P82226	hadronyche
800	2	6.9	36	1	Y16L_BPT4	P39244	bacterioph
801	2	6.9	36	1	Y297_ARCFU	O29945	archaeoglob
802	2	6.9	36	1	Y4KD_BPCHP	P19188	bacterioph
803	2	6.9	36	1	Y609_BORBU	O51554	borrelia bu
804	2	6.9	36	1	Y619_ARCFU	O29636	archaeoglob
805	2	6.9	36	1	Y699_TREPA	O83697	treponema p
806	2	6.9	36	1	YC12_CYAPA	P48256	cyanophora
807	2	6.9	36	1	YG50_HAEIN	P44281	haemophilus
808	2	6.9	36	1	YRKG_BACSU	P54434	bacillus su
809	2	6.9	37	1	24KD_PLACH	P14592	plasmodium
810	2	6.9	37	1	AFP4_MALPA	P83138	malva parvi
811	2	6.9	37	1	ANP3_PSEAM	P02733	pseudopleur
812	2	6.9	37	1	ATPO_SOLTU	P80504	solanum tub
813	2	6.9	37	1	B2MG_ORENI	Q03423	oreochromis
814	2	6.9	37	1	CAL1_PIG	P30880	sus scrofa
815	2	6.9	37	1	CEC2_MANSE	P14662	manduca sex

816	2	6.9	37	1	CEC3_MANSE	P14663	manduca sex
817	2	6.9	37	1	CEC4_MANSE	P14664	manduca sex
818	2	6.9	37	1	CG2S_LUPAN	P09930	lupinus ang
819	2	6.9	37	1	CS40_STAAU	P81684	staphylococ
820	2	6.9	37	1	CUP4_SARBU	P14486	sarcophaga
821	2	6.9	37	1	DEFA_MYTED	P81610	mytilus edu
822	2	6.9	37	1	ECAA_ECTTU	P49343	ectatomma t
823	2	6.9	37	1	ES2A_RANES	P40845	rana escule
824	2	6.9	37	1	ES2B_RANES	P40846	rana escule
825	2	6.9	37	1	F13A_BOVIN	P12260	bos taurus
826	2	6.9	37	1	GHR3_RAT	P33580	rattus norv
827	2	6.9	37	1	HCYB_CANPG	P83175	cancer pagu
828	2	6.9	37	1	HOXF_RHOOP	P22658	rhodococcus
829	2	6.9	37	1	LPPY_SERMA	P19937	serratia ma
830	2	6.9	37	1	MAUR_PARVE	Q56462	paracoccus
831	2	6.9	37	1	ME20_EUPRA	P26888	euplotes ra
832	2	6.9	37	1	MIBP_PSESP	P04576	pseudomonas
833	2	6.9	37	1	NLT3_VITSX	P80273	vitis sp. (
834	2	6.9	37	1	NLT4_VITSX	P80274	vitis sp. (
835	2	6.9	37	1	NUFM_SOLTU	P80266	solanum tub
836	2	6.9	37	1	OP2A_OXYKI	P83248	oxyopes kit
837	2	6.9	37	1	OP2B_OXYKI	P83249	oxyopes kit
838	2	6.9	37	1	OP2C_OXYKI	P83250	oxyopes kit
839	2	6.9	37	1	OP2D_OXYKI	P83251	oxyopes kit
840	2	6.9	37	1	PETG_ANASP	P58246	anabaena sp
841	2	6.9	37	1	PETG_ANAVA	Q913p7	anabaena va
842	2	6.9	37	1	PETG_ARATH	P56775	arabidopsis
843	2	6.9	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
844	2	6.9	37	1	PETG_CHLEU	P46304	chlamydomon
845	2	6.9	37	1	PETG_CHLRE	Q08362	chlamydomon
846	2	6.9	37	1	PETG_CHLVU	P56305	chlorella v
847	2	6.9	37	1	PETG_CUSRE	P30398	cuscuta ref
848	2	6.9	37	1	PETG_CYAPA	P14236	cyanophora
849	2	6.9	37	1	PETG_EUGGR	P30396	euglena gra
850	2	6.9	37	1	PETG_GUIITH	O78505	guillardia
851	2	6.9	37	1	PETG_MARPO	P12120	marchantia
852	2	6.9	37	1	PETG_MESVI	Q9mun3	mesostigma
853	2	6.9	37	1	PETG_NEPOL	Q9tky8	nephroselmi
854	2	6.9	37	1	PETG_ODOSI	P49470	odontella s
855	2	6.9	37	1	PETG_ORYSA	P12121	oryza sativ
856	2	6.9	37	1	PETG_PINTH	P41614	pinus thunb
857	2	6.9	37	1	PETG_PORPU	P51318	porphyra pu
858	2	6.9	37	1	PETG_PSINU	Q8wi02	psilotum nu
859	2	6.9	37	1	PETG_SKECO	O96811	skeletonema
860	2	6.9	37	1	PETG_SYNEL	Q8dki2	synechococc
861	2	6.9	37	1	PETG_SYNP7	Q9z3g1	synechococc
862	2	6.9	37	1	PIIL_ACHLY	P81720	achromobact
863	2	6.9	37	1	POLN_WEEV	P13896	western equ
864	2	6.9	37	1	PRF1_RAT	P18889	rattus norv
865	2	6.9	37	1	PSAI_ARATH	P56768	arabidopsis
866	2	6.9	37	1	PSAJ_EUGGR	P30394	euglena gra
867	2	6.9	37	1	PSBL_ARATH	P29301	arabidopsis
868	2	6.9	37	1	PSBL_ORYSA	P12166	oryza sativ
869	2	6.9	37	1	PSBM_PINTH	P41608	pinus thunb
870	2	6.9	37	1	PSBY_CYACA	O19893	cyanidium c
871	2	6.9	37	1	PSBY_GUIITH	O78433	guillardia
872	2	6.9	37	1	PYY_CHICK	P29203	gallus gall

873	2	6.9	37	1	REV_SIVM2	P08809	simian immu
874	2	6.9	37	1	RK36_ARATH	P12144	arabidopsis
875	2	6.9	37	1	RK36_ASTLO	P24355	astasia lon
876	2	6.9	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
877	2	6.9	37	1	RK36_CHLVU	P56360	chlorella v
878	2	6.9	37	1	RK36_CYACA	Q9tlu9	cyanidium c
879	2	6.9	37	1	RK36_CYAPA	P48131	cyanophora
880	2	6.9	37	1	RK36_EPIVI	P30069	epifagus vi
881	2	6.9	37	1	RK36_EUGGR	P21532	euglena gra
882	2	6.9	37	1	RK36_LOTJA	Q9bbq2	lotus japon
883	2	6.9	37	1	RK36_MARPO	P12142	marchantia
884	2	6.9	37	1	RK36_NEPOL	Q9tl126	nephroselmi
885	2	6.9	37	1	RK36_ODOSI	P49568	odontella s
886	2	6.9	37	1	RK36_OENHO	Q9mtj1	oenothera h
887	2	6.9	37	1	RK36_ORYSA	P12143	oryza sativ
888	2	6.9	37	1	RK36_PEA	P07815	pisum sativ
889	2	6.9	37	1	RK36_PINTH	P41631	pinus thunb
890	2	6.9	37	1	RK36_PORPU	P51296	porphyra pu
891	2	6.9	37	1	RK36_PSINU	Q8why9	psilotum nu
892	2	6.9	37	1	RK36_SPIOL	P12230	spinacia ol
893	2	6.9	37	1	RL36_ANASP	Q8ypk0	anabaena sp
894	2	6.9	37	1	RL36_AQUAE	O66487	aquifex aeo
895	2	6.9	37	1	RL36_BACHD	O50631	bacillus ha
896	2	6.9	37	1	RL36_BACST	P07841	bacillus st
897	2	6.9	37	1	RL36_BACSU	P20278	bacillus su
898	2	6.9	37	1	RL36_BORBU	O51452	borrelia bu
899	2	6.9	37	1	RL36_CAMJE	Q9pm84	campylobact
900	2	6.9	37	1	RL36_CLOAB	Q97ek2	clostridium
901	2	6.9	37	1	RL36_CLOPE	Q8xhu7	clostridium
902	2	6.9	37	1	RL36_DEIRA	Q9rsk0	deinococcus
903	2	6.9	37	1	RL36_HAEIN	P46361	haemophilus
904	2	6.9	37	1	RL36_HELPJ	Q9zjt1	helicobacte
905	2	6.9	37	1	RL36_HELPY	P56058	helicobacte
906	2	6.9	37	1	RL36_LEPIN	Q9xd13	leptospira
907	2	6.9	37	1	RL36_LISMO	Q927n0	listeria mo
908	2	6.9	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
909	2	6.9	37	1	RL36_MYCGE	P47420	mycoplasma
910	2	6.9	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
911	2	6.9	37	1	RL36_MYCPN	P52864	mycoplasma
912	2	6.9	37	1	RL36_MYCPU	Q98q05	mycoplasma
913	2	6.9	37	1	RL36_MYCSP	P38015	mycoplasma
914	2	6.9	37	1	RL36_MYCTU	P45810	mycobacteri
915	2	6.9	37	1	RL36_NEIMA	Q9jrb2	neisseria m
916	2	6.9	37	1	RL36_STAAM	Q99s42	staphylococ
917	2	6.9	37	1	RL36_STRCO	O86772	streptomyce
918	2	6.9	37	1	RL36_SYNP6	O24707	synechococc
919	2	6.9	37	1	RL36_THETH	P80256	thermus the
920	2	6.9	37	1	RL36_THETN	Q8r7x8	thermoanaer
921	2	6.9	37	1	RL36_TREPA	O83239	treponema p
922	2	6.9	37	1	RL36_UREPA	Q9pqn7	ureaplasma
923	2	6.9	37	1	RL36_VIBCH	P78001	vibrio chol
924	2	6.9	37	1	RL7_CLOPA	P05393	clostridium
925	2	6.9	37	1	RS15_HELLU	P52820	helix lucor
926	2	6.9	37	1	RUGC_RANRU	P80956	rana rugosa
927	2	6.9	37	1	SCIT_MESTA	P81761	mesobuthus
928	2	6.9	37	1	SCK2_LEIQH	P45628	leiurus qui
929	2	6.9	37	1	SCK3_BUTOC	P59290	buthus occi

930	2	6.9	37	1	SCK3_PARTR
931	2	6.9	37	1	SCKA_TITSE
932	2	6.9	37	1	SCKC_LEIQH
933	2	6.9	37	1	SMS_PETMA
934	2	6.9	37	1	TCTP_TRYBB
935	2	6.9	37	1	THHS_HORVU
936	2	6.9	37	1	TX21_SELHU
937	2	6.9	37	1	TX22_SELHU
938	2	6.9	37	1	TXD1_PARLU
939	2	6.9	37	1	TXD2_PARLU
940	2	6.9	37	1	TXD4_PARLU
941	2	6.9	37	1	TXJC_HADVE
942	2	6.9	37	1	TXKB_BUNGR
943	2	6.9	37	1	TXOF_HADVE
944	2	6.9	37	1	TXP3_APTSC
945	2	6.9	37	1	VA1_BPBF2
946	2	6.9	37	1	VG40_BPML5
947	2	6.9	37	1	VG65_BPPH2
948	2	6.9	37	1	VG65_BPPZA
949	2	6.9	37	1	VGJ_BPPHX
950	2	6.9	37	1	VP64_NPVBM
951	2	6.9	37	1	VPU_HV1Z8
952	2	6.9	37	1	Y268_ARCFU
953	2	6.9	37	1	Y63_BPT7
954	2	6.9	37	1	Y692_BORBU
955	2	6.9	37	1	Y700_BORBU
956	2	6.9	37	1	Y762_BORBU
957	2	6.9	37	1	Y846_BORBU
958	2	6.9	37	1	YBGT_ECOLI
959	2	6.9	37	1	YC12_CHLVU
960	2	6.9	37	1	YDA3_SCHPO
961	2	6.9	37	1	YIM4_BPPH1
962	2	6.9	37	1	YQGE_BACCA
963	2	6.9	37	1	YRYL_CAEEL
964	2	6.9	38	1	AFP5_MALPA
965	2	6.9	38	1	BD01_BOVIN
966	2	6.9	38	1	BD08_BOVIN
967	2	6.9	38	1	COA3_XANCP
968	2	6.9	38	1	CRS3_NOTGO
969	2	6.9	38	1	CU47_LACCU
970	2	6.9	38	1	DCHS_MICSP
971	2	6.9	38	1	DEF4_LEIQH
972	2	6.9	38	1	DEF7_SPIOL
973	2	6.9	38	1	DEFI_AESCY
974	2	6.9	38	1	DEFI_MYTGA
975	2	6.9	38	1	DLP3_ORNAN
976	2	6.9	38	1	DPOB_BOVIN
977	2	6.9	38	1	E2F1_RAT
978	2	6.9	38	1	EST5_DROMO
979	2	6.9	38	1	EXE1_HEL SU
980	2	6.9	38	1	FER_METPR
981	2	6.9	38	1	GLUM_HYDCO
982	2	6.9	38	1	GME1_RAT
983	2	6.9	38	1	H5_COLLI
984	2	6.9	38	1	HIS1_MACFA
985	2	6.9	38	1	HMG2_BOVIN
986	2	6.9	38	1	HOXH_RHOOP

P83112	parabuthus
P46114	tityus serr
P13487	leiurus qui
P21779	petromyzon
P35758	trypanosoma
P33045	hordeum vul
P82959	selenocosmi
P82960	selenocosmi
P83256	paracoelote
P83257	paracoelote
P83259	paracoelote
P82228	hadronyche
P29186	bunodosoma
P81599	hadronyche
P49268	aptostichus
P19347	bacterioph
Q05250	mycobacteri
P16515	bacterioph
P08384	bacterioph
P03651	bacterioph
P41722	bombyx mori
P08807	human immun
O29971	archaeoglob
P03799	bacterioph
O51635	borrelia bu
O51643	borrelia bu
O51703	borrelia bu
O51786	borrelia bu
P56100	escherichia
P56328	chlorella v
Q10345	schizosacch
P10428	bacterioph
P28753	bacillus ca
Q19177	caenorhabdi
P83139	malva parvi
P46159	bos taurus
P46166	bos taurus
Q07484	xanthomonas
P15534	nototodarus
P80323	lactobacill
P00863	micrococcus
P41965	leiurus qui
P81573	spinacia ol
P80154	aeschna cya
P80571	mytilus gal
P82141	ornithorhyn
Q27958	bos taurus
O09139	rattus norv
P10095	drosophila
P04203	heloderma s
P81542	metallospha
P23063	hydrolagus
Q9quz8	rattus norv
P02260	columba liv
P34084	macaca fasc
P40673	bos taurus
P22661	rhodococcus

987	2	6.9	38	1	ID5B_ADEPA	P09942 adenanthera
988	2	6.9	38	1	ID5B_PROJU	P32734 prosopsis j
989	2	6.9	38	1	MFA2_YEAST	P34166 saccharomyc
990	2	6.9	38	1	MUTS_YEREN	P47763 yersinia en
991	2	6.9	38	1	PA21_MATBI	P24644 maticora bi
992	2	6.9	38	1	PA22_MATBI	P24645 maticora bi
993	2	6.9	38	1	PACA_URAJA	P81039 uranoscopus
994	2	6.9	38	1	PERE_PIG	P80550 sus scrofa
995	2	6.9	38	1	PETG_SYNY3	P74149 synechocyst
996	2	6.9	38	1	POI_MUSDO	P81765 musca domes
997	2	6.9	38	1	PSAI_ODOSI	P49484 odontella s
998	2	6.9	38	1	PSAI_PROMA	O87786 prochloroco
999	2	6.9	38	1	PSAI_SYNEL	P25900 synechococc
1000	2	6.9	38	1	PSBF_TOBAC	P05171 nicotiana t

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.

AC P81175;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).

OS Rhamdia sapo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Pimelodidae; Rhamdia.

OX NCBI_TaxID=55673;

RN [1]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=98036128; PubMed=9370361;

RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,

RA Santome J.A.;

RT "Amino acid sequence, binding properties and evolutionary

RT relationships of the basic liver fatty-acid-binding protein from the

RT catfish Rhamdia sapo.";

RL Eur. J. Biochem. 249:510-517(1997).

CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: INTESTINE.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

DR InterPro; IPR000463; Fatty_acid_BP.

DR PROSITE; PS00214; FABP; PARTIAL.

KW Transport; Lipid-binding.

FT NON_TER 1 1

FT NON_CONS 12 13

FT NON_CONS 20 21

FT NON_CONS 28 29

FT NON_TER 33 33

SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 17.2%; Score 5; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 13 SVSEI 17

RESULT 2

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
AC P08377;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sarcotoxin IC.
OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7386;
RN [1]
RP SEQUENCE.
RX MEDLINE=85207747; PubMed=3888997;
RA Okada M., Natori S.;
RT "Primary structure of sarcotoxin I, an antibacterial protein induced
RT in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.";
RL J. Biol. Chem. 260:7174-7177(1985).
CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
DR PIR; C22625; CKFHCS.
DR InterPro; IPR000875; Cecropin.
DR InterPro; IPR003253; Sarctxn_cecrpn.
DR Pfam; PF00272; cecropin; 1.
DR ProDom; PD001670; Sarctxn_cecrpn; 1.
DR PROSITE; PS00268; CECROPIN; 1.
KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 13.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||||
Db 2 WLRK 5

RESULT 3

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.

AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROL OR GROEL OR MOPA.
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved Mycobacterium smegmatis.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chaprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

 Query Match 10.3%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 18 LNS 20

RESULT 4

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
 AC P80499;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;

RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria."
 RL Plant J. 9:357-368(1996).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAF79E2682849C CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 5

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases."
 RL FEBS Lett. 414:359-361(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28

SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 7 EWL 9

RESULT 6

PA23_TRIST

ID PA23_TRIST STANDARD; PRT; 28 AA.
AC P82894;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
OS Trimeresurus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=39682;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Li S.Y., Wang W.Y., Xiong Y.L.;
RT "Isolation, sequence and characterization of five variants of
RT phospholipase A2 from venom of snake Trimeresurus stejnegeri."
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic
CC activities are not detected.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
CC SUBFAMILY.
DR HSSP; P82287; 1QLL.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||

Db

5 LGK 7

RESULT 7

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
AC P20260;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
DE 2-acylhydrolase) (Fragment).
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=89388835; PubMed=2675391;
RA Schmidt J.J., Middlebrook J.L.;
RT "Purification, sequencing and characterization of pseudexin
RT phospholipases A2 from Pseudechis porphyriacus (Australian
RT red-bellied black snake).";
RL Toxicon 27:805-818(1989).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
CC SUBFAMILY.
DR PIR; C32416; C32416.
DR HSSP; P00592; 2PHI.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAA0D5 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
|||
Db 3 IQL 5

RESULT 8

VI03_VACCP

ID VI03_VACCP STANDARD; PRT; 28 AA.

AC Q00334;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Protein I3 (Fragment).
 GN I3L.
 OS Vaccinia virus (strain L-IVP).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=31531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91066899; PubMed=2250685;
 RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
 RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
 RA Malygin E.G.;
 RT "Molecular-biological study of vaccinia virus genome. II.
 RT Localization and nucleotide sequence of vaccinia virus genes coding
 RT for proteins 36K and 12K.";
 RL Mol. Biol. (Mosk) 24:968-976(1990).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
 CC THE LATE PHASE OF INFECTION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; X61165; CAA43473.1; -.
 DR InterPro; IPR006754; Pox_I3.
 DR Pfam; PF04661; Pox_I3; 1.
 KW Early protein; Late protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
 |||
 Db 5 NLG 7

RESULT 9
 VIP_ALLMI
 ID VIP_ALLMI STANDARD; PRT; 28 AA.
 AC P48142; P01285;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 10

VIP_RANRI

ID VIP_RANRI STANDARD; PRT; 28 AA.
 AC P81016;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 11

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.
 AC P04565;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Ovis aries (Sheep),
 OS Capra hircus (Goat), and
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940, 9925, 9615;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Brain;
 RX MEDLINE=91045331; PubMed=2235680;
 RA Gafvelin G.;
 RT "Isolation and primary structure of VIP from sheep brain.";
 RL Peptides 11:703-706(1990).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Small intestine;
 RX MEDLINE=91239834; PubMed=2034821;
 RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
 RA Christophe J.;
 RT "Purification and amino acid sequence of vasoactive intestinal
 RT peptide, peptide histidine isoleucinamide and secretin from the ovine
 RT small intestine.";
 RL Regul. Pept. 32:169-179(1991).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=C.hircus, and C.familiaris;
 RX MEDLINE=86313167; PubMed=3748846;
 RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
 RT "Purification and amino acid sequences of dog, goat and guinea pig

RT VIPs.";
 RL Peptides 7 Suppl. 1:17-20(1986).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60304; A60304.
 DR PIR; B60072; VRSH.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 10.3%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 12

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
 AC P11530;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dystrophin (Fragment).
 GN DMD.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122671; PubMed=3340214;
 RA Nudel U., Robzyk K., Yaffe D.;
 RT "Expression of the putative Duchenne muscular dystrophy gene in
 RT differentiated myogenic cell cultures and in the brain.";
 RL Nature 331:635-638(1988).
 CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
 CC plasma membrane.
 CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
 CC and SNTG2 (By similarity).

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DR EMBL; X07000; CAA30057.1; -.
DR PIR; S01614; S01614.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR PROSITE; PS00019; ACTININ_1; PARTIAL.
DR PROSITE; PS00020; ACTININ_2; PARTIAL.
DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQ 29
|||
Db 12 KLQ 14

RESULT 13

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
AC P47215;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95023390; PubMed=7524049;
RA Wang Y., Conlon J.M.;
RT "Purification and primary structure of galanin from the alligator
RT stomach.";
RL Peptides 15:603-606(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.

FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 14

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95083480; PubMed=7527531;
RA Wang Y., Conlon J.M.;
RT "Purification and characterization of galanin from the
RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
RT (*Scyliorhinus canicula*).";
RL Peptides 15:981-986(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 15

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
 AC P30802;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 16

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 17

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 18

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
 AC P31234;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN OR GLNN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92158824; PubMed=1724081;
 RA Sillard R., Langel U., Joernvall H.;
 RT "Isolation and characterization of galanin from sheep brain.";
 RL Peptides 12:855-859(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17

|||

Db 4 LNS 6

RESULT 19

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.

AC P31297;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glucagon.

GN GCG.

OS Chinchilla brevicaudata (Chinchilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;

OC Chinchilla.

OX NCBI_TaxID=10152;

RN [1]

RP SEQUENCE.

RX MEDLINE=91045327; PubMed=2235678;

RA Eng J., Kleinman W.A., Chu L.S.;

RT "Purification of peptide hormones from chinchilla pancreas by

RT chemical assay.";

RL Peptides 11:683-685(1990).

CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.

CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

DR PIR; A60413; GCCB.

DR HSSP; P01275; 1BH0.

DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 1.

DR PRINTS; PR00275; GLUCAGON.

DR SMART; SM00070; GLUCA; 1.

DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Hormone.

SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15

|||

Db 12 KHL 14

RESULT 20

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.

AC P19371;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase) (Fragment).
 OS *Desulfovibrio vulgaris* (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from *Desulfovibrio vulgaris*: rubrerythrin
 RT and a new, highly active, enzyme."
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 21

NUO1_SOLTU
 ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS *Solanum tuberosum* (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,

RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT *Solanum tuberosum*.";
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
 |||
 Db 2 RKK 4

RESULT 22

P2SM_LOXIN

ID P2SM_LOXIN STANDARD; PRT; 29 AA.
 AC P83046;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).
 OS *Loxosceles intermedia* (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
 OX NCBI_TaxID=58218;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR
 RP LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Venom;
 RX MEDLINE=99009277; PubMed=9790962;
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;
 RT "Sphingomyelinases in the venom of the spider *Loxosceles intermedia*
 RT are responsible for both dermonecrosis and complement-dependent
 RT hemolysis.";
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-
 CC dependent hemolysis and dermonecrosis.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.
 CC -!- COFACTOR: Calcium ion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

KW Hydrolase; Toxin; Calcium; Hemolysis.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 25 NLG 27

RESULT 23

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 24

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7P (Fragment).
 GN RPS7P OR S7.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens.";
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 25

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.

AC P80740;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e

DE V) (Fragment).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea."
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.
 DR Pfam; PF00080; sodcu; 1.
 DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 7 LNS 9

RESULT 26

TL16_SPIOL

ID TL16_SPIOL STANDARD; PRT; 29 AA.
 AC P81834;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=98175931; PubMed=9506969;
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
 RT "The thylakoid lumen of chloroplasts. Isolation and
 RT characterization.";

RL J. Biol. Chem. 273:6710-6716(1998).
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 27

DMS3_PHYSA

ID DMS3_PHYSA STANDARD; PRT; 30 AA.
AC P80279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 3 (DS III).
OS Phyllomedusa sauvagei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=94139686; PubMed=8306981;
RA Mor A., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin."
RL Eur. J. Biochem. 219:145-154(1994).
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 23 KKL 25

RESULT 28

FTN_BACFR

ID FTN_BACFR STANDARD; PRT; 30 AA.

AC P28733;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from Bacteroides fragilis."
 RL FEMS Microbiol. Lett. 74:207-212(1992).
 CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 29

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.

AC P11726;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
 DE (Fragment).
 OS Aeromonas punctata (Aeromonas caviae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OX NCBI_TaxID=648;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIB 9232;

RX MEDLINE=85104799; PubMed=3968036;
 RA Falmagne P., Portetelle D., Stalon V.;
 RT "Immunological and structural relatedness of catabolic ornithine
 RT carbamoyltransferases and the anabolic enzymes of enterobacteria.";
 RL J. Bacteriol. 161:714-719(1985).
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
 CC + L-citrulline.
 CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 DR InterPro; IPR006130; Asp/Orn_COtranf.
 DR InterPro; IPR006132; OTCace_P.
 DR Pfam; PF02729; OTCace_N; 1.
 DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
 KW Transferase; Arginine metabolism.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
 |||
 Db 19 EIQ 21

RESULT 30

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
 AC P82415;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ponericin G2.
 OS Pachycondyla goeldii (Ponerine ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; Pachycondyla.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P.; Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant Pachycondyla goeldii.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 31

PCG3_PACGO

ID PCG3_PACGO STANDARD; PRT; 30 AA.
AC P82416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G3.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 32

PSAM_PORPU

ID PSAM_PORPU STANDARD; PRT; 30 AA.
AC P51395;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Photosystem I reaction centre subunit XII (PSI-M).
GN PSAM.

OS Porphyra purpurea.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TaxID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RA Reith M.E., Munholland J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
 RT genome.";
 RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
 CC -----
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 CC -----
 DR EMBL; U38804; AAC08281.1; -.
 DR PIR; S73316; S73316.
 KW Photosystem I; Photosynthesis; Chloroplast.
 SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
 |||
 Db 24 LGK 26

RESULT 33

TX2_THRPR
 ID TX2_THRPR STANDARD; PRT; 30 AA.
 AC P83476;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Toxin ProTx-II.
 OS Thrixopelma pruriens (Green velvet).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Thrixopelma.
 OX NCBI_TaxID=213387;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
 RP SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=22363233; PubMed=12475222;
 RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
 RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,
 RA Mehl J.T., Cohen C.J., Smith M.M.;
 RT "Two tarantula peptides inhibit activation of multiple sodium
 RT channels.";

RL Biochemistry 41:14734-14747(2002).
 CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
 CC Shifts the voltage-dependence of channel activation to more
 CC positive potentials.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
 CC TOXIN FAMILY.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
 KW Sodium channel inhibitor.
 FT DISULFID 2 16
 FT DISULFID 9 21
 FT DISULFID 15 25
 SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

 Query Match 10.3%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 27 KKL 29

RESULT 34

UP61_UPEIN

ID UP61_UPEIN STANDARD; PRT; 30 AA.
 AC P82037;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 6.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata."
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 35

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
AC P82038;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.2.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 36

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
AC Q04238;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
DE (Fragment).
OS Equisetum arvense (Field horsetail) (Common horsetail).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
OX NCBI_TaxID=3258;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=93138084; PubMed=8422915;
RA Starke T., Gogarten J.P.;
RT "A conserved intron in the V-ATPase A subunit genes of plants and
RT algae.";
RL FEBS Lett. 315:252-258(1993).
CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
CC CELLS.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
CC V-ATPASE SUBUNIT IN PSILLOTUM AND EQUISETUM.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
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CC -----
DR EMBL; X56984; CAA40302.1; -.
DR PIR; S21815; S21815.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW Multigene family.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MER 20
|||
Db 23 MER 25

RESULT 37
Y523_BORBU
ID Y523_BORBU STANDARD; PRT; 30 AA.
AC O51473;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein BB0523.
GN BB0523.
OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";
 RL Nature 390:580-586(1997).

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 CC -----

DR EMBL; AE001154; AAC66894.1; -.
 DR PIR; B70165; B70165.
 DR TIGR; BB0523; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 26 ERV 28

RESULT 38

CEC1_PIG

ID CEC1_PIG STANDARD; PRT; 31 AA.
 AC P14661;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cecropin P1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90083227; PubMed=2512577;
 RA Lee J.-Y., Boman A., Chuanxin S., Andersson M., Joernvall H., Mutt V.,

RA Boman H.G.;
 RT "Antibacterial peptides from pig intestine: isolation of a mammalian
 RT cecropin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9159-9162(1989).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93011123; PubMed=1396696;
 RA Sipos D., Andersson M., Ehrenberg A.;
 RT "The structure of the mammalian antibacterial peptide cecropin P1 in
 RT solution, determined by proton-NMR.";
 RL Eur. J. Biochem. 209:163-169(1992).
 CC -!- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST
 CC SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. ACTS BY A
 CC NONPORE MECHANISM.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
 DR PIR; A36221; A36221.
 DR InterPro; IPR000875; Cecropin.
 DR Pfam; PF00272; cecropin; 1.
 DR PROSITE; PS00268; CECROPIN; 1.
 KW Antibiotic.
 SQ SEQUENCE 31 AA; 3339 MW; CB2B374A8B153850 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 8 KKL 10

RESULT 39

CXMA_CONMR

ID CXMA_CONMR STANDARD; PRT; 31 AA.
 AC P56708;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mu-O-conotoxin MrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RX MEDLINE=95348106; PubMed=7622492;
 RA McIntosh J.M., Hasson A., Spira M.E., Gray W.R., Li W., Marsh M.,
 RA Hillyard D.R., Olivera B.M.;
 RT "A new family of conotoxins that blocks voltage-gated sodium
 RT channels.";
 RL J. Biol. Chem. 270:16796-16802(1995).
 CC -!- FUNCTION: Mu-O-conotoxins bind and block voltage-sensitive sodium
 CC channel (VSSC).
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=3487.8; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. MU-O-TYPE
 CC FAMILY.
 DR PIR; A58586; A58586.
 KW Toxin; Sodium channel inhibitor.
 FT DISULFID 2 20 BY SIMILARITY.
 FT DISULFID 9 25 BY SIMILARITY.
 FT DISULFID 19 30 BY SIMILARITY.
 SQ SEQUENCE 31 AA; 3495 MW; 741FA610E6F9D289 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
 |||
 Db 3 RKK 5

RESULT 40

DEJP_DROME

ID DEJP_DROME STANDARD; PRT; 31 AA.
 AC P81160;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ductus ejaculatorius peptide 99B.
 GN DUP99B.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE OF 1-24 FROM N.A., AND SEQUENCE OF 9-31.
 RC STRAIN=Oregon-R; TISSUE=Ductus ejaculatorius;
 RX MEDLINE=21835775; PubMed=11846801;
 RA Saudan P., Hauck K., Soller M., Choffat Y., Ottiger M., Sporri M.,
 RA Ding Z., Hess D., Gehrig P.M., Klauser S., Hunziker P., Kubli E.;
 RT "Ductus ejaculatorius peptide 99B (DUP99B), a novel Drosophila
 RT melanogaster sex-peptide pheromone.";
 RL Eur. J. Biochem. 269:989-997(2002).
 CC -!- FUNCTION: INDUCES POST-MATING RESPONSES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: DUCTUS EJACULATORIUS.
 CC -!- SIMILARITY: TO PARAGONIAL PEPTIDE B.
 DR FlyBase; FBgn0024381; Dup99B.
 DR GO; GO:0045434; P:negative regulation of female receptivity, . . .; IMP.
 DR GO; GO:0046662; P:regulation of oviposition; NAS.
 KW Behavior; Glycoprotein; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 19 31
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 31 AA; 3766 MW; B90A9B99C120EF49 CRC64;

Query Match 10.3%; Score 3; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 22 NLG 24

Search completed: January 14, 2004, 10:35:38
Job time : 6.78816 secs